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CNABRWYSLWYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60

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		28	943	100.0	487	н,	US-08-557-287-2	287-2	Sequence	2, Appli
		5 C	943	100.0	487		US-08-470-366-2 US-08-261-660A-12	366-2 660A-12	Sequence	
		31	943	100.0	487	1 ~1	US-08-209-762-69	762-69	Sequence	
		32	943	100.0	487	7	US-08-644-290-2	290-2	Sequence	2, Appli
		33	943	100.0	487	٦,	US-08-378-228-2	228-2	Sequence	2, Appli
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accolds		9 0	943	100.0	487		US-08-274-303-2	303-2	Sequence	
updates/sec		37	943	100.0	487	-	US-07-915-720D-13	720D-13	Seguence	13, Appl
		38	943	100.0	487	н,	US-08-218-026-4	026-4	Sequence	
		J 2	44.0	100.0	404	⊣ ເ	US-08-435-855-7	2-008	Sequence	2, Appli
184 TANK		* 4 > -	44.0	000	487	4 C	TIS-08-653-632-4	632-4	Sequence	4
PINT TO		4.2	943	0.00	487	٥ د	US-08-466-624-2	624-2	Sequence	
		1 4 1 6	943	100.0	487	1 (1	US-08-621-803-265	803-265	Sequence	265, App
		4	943	100.0	487	~	US-08-466-826-2	826-2	Sequence	ς,
		45	943	100.0	487	7	US-08-704-504-2	.504-2	Sequence	2, Appli
							ALIGNMENTS	SINTS		
	RE US	RESULT 1 US-07-915-720D-16	720D-1	91						
		Sequence 16, Application US/07915720D	16, 7	Applica	tion U	5/07	915720D			
	. ••	Patent Nos. 5770694	05.57	70694	_					
	•	GENERAL INFORMATION:	INFO	RMATION	.,	:				
	•	APPLI	APPLICANT:		, Rand	3 2				
		TITLE	AFFLICANI: TITLE OF IN	15	Ē.	NETI	CALLY ENGIN	GENETICALLY ENGINEERED BPI VARIANT	ARIANT	
	• •	TITLE	G G	TITLE OF INVENTION:		PROTEINS	NS			
		NUMBE	R OF	NUMBER OF SEQUENCES:	ES: 27	7				
	••	CORRE	SPOND	CORRESPONDENCE ADDRESS:	DRESS:					
	••	AD S	RESSE	ADDRESSEE: Fish & Richardson,	h & Ri	char	ADDRESSEE: Fish & Richardson, P.C.	00.		
		A F	. 1 . A	Menlo Dark	מוום גוי	4	סמת' פתדרם	201		
have a	• ••	STA	STATE: (5	:					
ing printed,	· ••	CO	COUNTRY:	USA						
·	•-	ZIP:	: 94	94025						
	•	COMPO	TER K	COMPUTER READABLE FORM:	FORM:	:				

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Sequence 9146, Application US/09949016

Patent No. 6812339
GENERAL INPORMATION:
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activity for Gram
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
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APPLICANT: Gray, Beulah
APPLICANT: Maseman, Judith R.
APPLICANT: Mayo, Kevin
TITLE OF INVENTION: Synthetic Peptides with Bactericidal
TITLE OF INVENTION: Activity and Endotoxin Neutralizing Activity fo.
TITLE OF INVENTION: Activity and Endotoxin Neutralizing Activity fo.
TITLE OF INVENTION: Beative Bacteria and Methods for Their Use
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5786324west Center
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 943; DB 4; Length 262; 100.0%; Pred. No. 5.1e-70; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08218026
; Patent No. 5786324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 184; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                             RESULT 3
US-09-949-016-9146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-218-026-2
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                        KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
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DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCOLE, Randal W.
APPLICANT: Marra, Marian N.
TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: BOALCOVIC & Reed, LLP
STREET: 285 Hamilton, Suite 200
CITY: Palo Alco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,543
FILNG DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: Francis, Carol L:
REGISTRATION NUMBER: 36,513
REGISTRATION NUMBER: 36,513
RELEFANCE FOOCKET NUMBER: 36,513
TELEFHONE: 650/327-3400
TELEFANCE 650/327-3400
TELEFANCE 650/327-3323
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
FUNCTH: 243 amilno acids
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100.0%; Pred. No. 4.7e-70;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      US-09-025-543-16
; Sequence 16, Application US/09025543
; Patent No. 6093801
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
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Best Local Similarity 100.
Matches 184; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/07915720D
; Sequence 15, Application US/07915720D
; Patent No. 5770694
; GENERAL INFORMATION:
    APPLICANT: Scott, Randal W.
    APPLICANT: Marra, Marian N.
    TITLE OF INVENTION: ENGINEERED BPI VARIANT
    TITLE OF INVENTION: PROTEINS
    NUMBER OF SEQUENCES: 27
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson, P.C.
    STREET: 2200 Sand Hill Road, Suite 100
    CONTY: Marian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/915,720D
FILING DATE: 22-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L.
REGISTRATION NUMBER: 06514/03001
TELECOMMULCATION INFORMATION:
TELEPHONE: 415/832-5070
TELEPA: 415/832-5070
TELEPA: 415/832-6075
TELEPA: 415/832-6075
TELEPA: 415/832-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
TELEFAX: 612/332-9081
                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 300 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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US-07-915-720D-15
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APPLICANT: GRAY, Beulah
APPLICANT: HASEMAN, Judith R.
APPLICANT: HASEMAN, Judith R.
APPLICANT: MAYO, Kevin
TITLE OF INVENTION: PEPTIDES WITH BACTERICIDAL AND ENDOTOXIN NEUTRALIZING
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 5830860west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 129
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CUCHAITS
CUCHAITS
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,632
FILING DATE: 24-MAY-1996
CLASSIFICATION NUMBER: 08/218026
FILING DATE: 24-MAY-1996
APPLICATION NUMBER: 08/218026
FILING DATE: 24-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Domise
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.286USII
                     PELLICATION NUMBER: US/08/218,026
FILING DATE: 24-MAR-1994
CLASSIPICATION NUMBER: US/08/218,026
FILING DATE: 24-MAR-1994
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KOWALCHY, KATHOFTION
FEGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 36,848
FELECOMMUNICATION NUMBER: 36,086 US01
TELEPHONE: 612-332-9081
FELEPAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-08-218-026-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08653632 Patent No. 5830860
        CURRENT APPLICATION DATA:
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STATE: MR
COUNTRY:
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Therapeutic uses of Bactericidal/Permeability-Increasing Protein Products
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                                                                                      DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
                                                                                                                                                                121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
             CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60
                                     10 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCarthy, Sean A
APPLICANT: McCarthy, Sean A
APPLICANT: Barnes, Thomas M
APPLICANT: Barnes, Thomas M
APPLICANT: Share, Christopher C
APPLICANT: Share, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
FILE REPERENCE: 210147,0023/6/11
CURRENT APPLICATION NUMBER: US/09/578,063
CURRENT FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 79
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Patent No. 5348942

GENERAL INFORMATION:
APPLICANT: Little, Roger G. II
APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Parent, James Brian
ITILE OF INVENTION: Bactericidal/Perm
                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/09578063
Patent No. 6764677
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Ver. 2.1
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Best Local Similarity 100.
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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SEQ ID NO 38
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                                                                                                                                 Length 368;
                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09025543
Patent No. 6093801
GENERAL INFORMATION:
APPLICANT: Scott, Randal W.
APPLICANT: Marra, Marian N.
TITLE OF INVENTION: GENERICALLY ENGINEERED BPI VARIANT
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,543
FLING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L.
REGISTRATION NUMBER: 36,513
REGISTRATION NUMBER: 06514/030005
TELECHONE: 650/327-3400
                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 184; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 285 Hamilton, Suite 200 CITY: Palo Alto
             TYPE: amino acid
STRANDEDNESS: not relevant
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368 amino acida
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Best Local Similarity 100.
Matches 184; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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                                                                                        US-07-915-720D-15
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US-09-025-543-15
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DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
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                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Batenitn Release #1.0, Version #1.25
SOFTWARE: Patenitn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/013,801
FILING DATE: US PEB 1993
CLASSIFICATION: 424
ATTONENTY/AGENT INPORMATION:
NAME: MAYERS THOWAS P.36,989
REGISTRATION NUMBER: P.36,989
REGISTRATION NUMBER: P.36,989
TELEROMAUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEROMS: 312/346-5740
                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 487 amino acids TYPE: amino acid
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Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 HKKI 184
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US-08-013-801-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08013801
; Sequence 2, Application US/08013801
; Patent No. 5420019
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
APPLICANT: Burke, David
APPLICANT: Baltaian, Manik
APPLICANT: Baltaian, Lynn S
TITLE OF INVENTION: Stable Bactericidal/Permeability-
TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical
TITLE OF INVENTION: Compositions Containing the Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
; STREET: Two First National Plaza
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
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                                          8: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                    OFFWALE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,644
FILING DATE: 19930312
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 31229
TELEPHONE: 312/44-6300
TELEPHONE: 312/44-6300
TELEPHONE: 312/44-048
                                                                                                                                      ZIP: 60606-6402
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                       CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                            ADDRESSEE:
STREET: 63
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity
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Patent No. 5447913
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
APPLICANT: Ammons, William Steve
TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
TITLE OF INVENTION: Increasing Protein Dimer Products
NUMBER OF SEQUENCES: 11
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: F0606-6402
COMPUTER: F100Py disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,132
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 943; DB 1;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0;
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      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 30655
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEFAX: 312/474-6448
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: AMINO ACID
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NAME: Sharp, Jeffrey S.
REGISTATION UNDRER: 31,879
REFERENCE/DOCKET UNDRER: 2712:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEFAX: 25-3856
  19930519
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-072-063-2
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70 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 129
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                                                                                                                                                                    Query Match
100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels
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APPLICANT:
APPLICANT:
TITLE OF INVENTION: Method of Treating Conditions
TITLE OF INVENTION: Associated With Burn Injuries
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,924
FILING DATE:
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TELECOMONICATION INFORMATION:
TELEPHONE: 312/474-6100
TELEFRAX: 312/474-0448
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5494896
GENERAL INFORMATION:
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NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                         : 487 amino acids
amino acid
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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Indels

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61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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                                                                                                                                                                                                                                                                    10 CNAPRHVSLAMLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDVS
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                                                                   1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cohen, Jonathan
APPLICANT: Kung, Ada H.C.
APPLICANT: Kung, Ada H.C.
APPLICANT: Lambert, Jr., Lewis H.
TITLE OF INVENTION: Machod for Treating Gram-Negative Bacterial
TITLE OF INVENTION: Infection by Administration of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/311,611A
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100.0%; Pred. No. 9.9e-70;
iive 0; Mismatches 0;
100.0%; Pred. No. 9.9e-70; ive 0; Mismatches 0;
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Patent No. 5523288
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,401
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,651
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
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INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION:
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amino acid
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  Best Local Similarity 100.
Matches 184; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                      KASGNPDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 189
                                                                                          69
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                                                                        10 CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQCGTAALQKELKRIKIFDYS
                                                CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cohen, Jonathan
APPLICANT: Cohen, Jonathan
APPLICANT: Cohen, Jonathan
APPLICANT: Lambert, Jr., Lewis H.
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
TITLE OF INVENTION: Infection by Administration of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6100 Sears Tower, 233 South Wacker Drive
CITY: Chicago
CITY: Chicago
      0; Gaps
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      0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,611A
      0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,401
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,651
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 69, Application US/08311611A
Patent No. 5523288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 3225:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
OTHER INFORMATION: "rBPI"
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
    184; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                               HKKI 193
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US-08-311-611A-69
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                  181 HKKI 184
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Search completed: October 21, 2005, 11:32:58 Job time : 18.8241 secs

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61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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| Patent No. 5439807
| GENERAL INFORMATION:
| APPLICANT: Theofan, Georgia APPLICANT: Grinna, Lynn S
| APPLICANT: Horvatz, Arnold APPLICANT: OF INVENTION: BPI-Immunoglobulin Fusion Proteins NUMBER OF SEQUENCES: 18
| CORRESPONDENCE ADDRESS: ABSTRAIL O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indela
                                                                                                                                       OPERATING SYSTEM: EL-DOS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/013,801
FILING DATE: 02 FEB 1993
CLASSIFICATION: 424
ATTONERY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 27,129/30911
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: 312/346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 6066-6402
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 943; DB 1;
100.0%; Pred. No. 9.9e-70;
trive 0; Mismatches 0;
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEEX: 312/346-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
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Matches 184; Conservative
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STATE: Illlinois
Illinois
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Sequence 2, Application US/08013801

Setent No. 5420019

GENERAL INFORMATION:

APPLICANT: Theofan, Georgia

APPLICANT: Burke, David

APPLICANT: Burke, David

APPLICANT: Burke, David

APPLICANT: Burke, David

TITLE OF INVENTION: Stable Bactericidal/Permeability-

TITLE OF INVENTION: Compositions Containing the Same

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bicknell

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CNAPRWVSLMVLVALGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
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                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Plopy disk
COMPUTER: 1BM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,644
FILING DATE: 19930312
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 31,879
TELEPRAK: 312,474-6300
TELEPRAK: 312,474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 487 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
      NUMBER OF SEQUENCES:
                                                                                    CITY: Chicase
STATE: Illinois
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October 21, 2005, 11:22:43; Search time 47.1759 Seconds (without alignments) 770.608 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                       OM protein - protein search, using sw model
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US-10-629-516-2 2507 1 MRENMARGPCNAPRWVSLMV........NVVLQPHQNFILLFGADVVYK 487

BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table:

513545 segs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* . .. 9 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9

1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL

g 8

Sequence 2, Appli Sequence 252, Appli Sequence 252, Appli Sequence 252, Appli Sequence 252, Appli Sequence 2, Appli
US-08-274-303-2 US-07-915-720D-13 US-08-465-855-2 US-08-466-624-2 US-08-466-624-2 US-08-466-624-2 US-08-466-624-2 US-08-465-485-45A-69 US-08-704-504-2 US-08-621-259A-252 US-08-621-259A-252 US-08-621-259A-252 US-08-621-259A-252 US-08-621-259A-252 US-09-081-166-2 US-09-081-166-2 US-09-091-156-2
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ALIGNMENTS

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; Sequence 2, Application US/08030644
; Sequence 2, Application US/08030644
; Patent No. 5348942
; GENERAL INFORMATION:
    APPLICANT: Little, Roger G. II
    APPLICANT: Parent, James Brian
    TITLE OF INVENTION: Therapeutic uses of
    TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Products
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
    STREE: 6300 Sears Tower, 233 South Wacker Drive
    CITY: Chicago
    STATE: Illinois
    COUNTRY: USA.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONEY/AGENT INPOMENTION:
NAME:
ATTONEY/AGENT INPOMENTION:
NAME:
REGISTRATION NUMBER:
31,879
REGISTRATION NUMBER:
31,299
REGISTRATION NUMBER:
TELECOMMUNICATION INPORMER:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2507; DB 1;
100.0%; Pred. No. 6.6e-209;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              ZIP: 60606-6402
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
TOPOLOGY: 14-
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Best Local Similarity 100.
Matches 487; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312/474-0448
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us-10-629-516-2.rai

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RESULT 3
US-08-072-063-2
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KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG 120
                                                                240
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                                                                                                                                                                                                    VAPPATTAETLDVQMKGEFYSENHHNPPPPRAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV 300
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                                                                                                                                                                                                                                                                                                                    PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
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                                                                                                                 KVGWLIQLFHKKIESALRNKANSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
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Sequence 2, Application US/08013801
Sequence 2, Application US/08013801
Sequence 3, Application US/08013801
Sequence 3, Application US/08013801
Sequence 3, Application US/08013801
Sequence 4, Arcold Applicant: Theofar: Burke, David Applicant: Baltaian, Manik Applicant: Baltaian, Manik Applicant: Grinna, Lynn S 1717LE OF INVENTION: Labele Bactericidal/Permeability-1717LE OF INVENTION: Increasing Protein Products and Pharmaceutical 1717LE OF INVENTION: Compositions Containing the Same NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/013,801
FILING DATE: 02 FEB 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two First National Plaza CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 27128
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312/346-9740
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TELEX: 25-3856
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South Wacker
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APPLICANT: Theofan, Georgia
APPLICANT: Grinna, Lynn S
APPLICANT: Grinna, Lynn S
APPLICANT: Grinna, Lynn S
APPLICANT: Horwitz, Arnold
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
UNDMER OF SEQUENCES: 18
CORRESPONDENCES ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Born
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,063
                                                                                                                                                                               100.0%; Score 2507; DB 1;
100.0%; Pred. No. 6.6e-209;
:Ive 0; Mismatches 0;
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    7
                                          LENGTH: 487 amino acide
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 487; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 GADVVYK 487
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STATE: Illlinois
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RY: United States of America 60606-6402
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US-08-414-924-2
'Sequence 2, Application US/08414924
'Patent No. 5494896
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 487; Conservative
                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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US-08-212-132-2
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APPLICANT: Little Roger G.
APPLICANT: Anmons, William Steve
TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
TITLE OF INVENTION: Increasing Protein Dimer Products
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
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                                                                                                                                                                                                                                                             Length 487;
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100.0%; Pred. No. 6.6e-209.
iive 0; Mismatches 0;
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          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers Thomas 76,989
REFERENCE/DOCKET NUMBER: 36,989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6448
                                                                                                              TELEFAX: 312/474-0448
TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 487 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                          Matches 487; Conservative
 FILING DATE: 19930519
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US-08-212-132-2
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181 KVGWLIQLFHKKIESALRNKONSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL 240
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMB PC compatible
COMPUTER: EMB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,132
FILING DATE:
FLING DATE:
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Sharty Jeffrey 31,879
REGISTRATION NUMBER: 31,879
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 104744-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2507; DB 1;
100.0%; Pred. No. 6.6e-209;
tive 0; Mismatches 0;
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9 9

180

240

300

180

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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    US-08-311-611A-69
; Sequence 69, Application US/08311611A
; Patent No. 5523288
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OTHER INFORMATION: "rBPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                         481 GADVVYK 487
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GENERAL INFORMATION:
APPLICANT: Hansbrough, John F.
TITLE OF INVENTION: Method of Treating Conditions
TITLE OF INVENTION: Associated With Burn Injuries
NUMBER OF SEQUENCES: 2
CORRESPEDNDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 1111nois
COUNTRY: United States of America
ZIP: 6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,924
FILING DATE:
FLING DATE:
REFERENCE/DOCKET NUMBER: 31,879
REGISTRATION NUMBER: 31,879
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 312/474-6408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
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Matches 487; Conservative
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MOLECULE TYPE: protein
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GENERAL INFORMATION:

APPLICANT: Cohen, Jonathan

APPLICANT: Cohen, Jonathan

APPLICANT: Cohen, Jonathan

APPLICANT: Cohen, Jonathan

APPLICANT: Lambert, J. B.

TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial

TITLE OF INVENTION: Infection by Administration of

TITLE OF INVENTION: Bactericidal/Permeability-Increasing

TITLE OF INVENTION:
NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,611A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,401
FILING DATE: 11-JUJ-1994
PRIOR APPLICATION NUMBER: 08/125,651
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REFERENCE/POCKET NUMBER: 31,879
REFERENCE/POCKET NUMBER: 31,879
REFERENCE/POCKET NUMBER: 3251
TELECOMMUNICATION NUMBER: 3251
TELECOMMUNICATION NUMBER: 3251
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Sequence 2, Application US/08173968
Patent No. 5576292
GENERAL INFORMATION:
                                                          Query Match

Best Local Similarity 100.0%;

Matches 487; Conservative 0

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-611A-146

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                                                                                                                                                                      PIGLIFYPAVDVQAFAVLPNSSLASLFLIGMHTIGSMEVSAESNRLVGELKLDRLLLELK 420
121 KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180
                                              PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cohen, Jonathan
APPLICANT: Cohen, Jonathan
APPLICANT: Kung, Ada H.C.
APPLICANT: Lambert, Jr., Lewis H.
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
TITLE OF INVENTION: Infection by Administration of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing
TITLE OF INVENTION:
TITLE OF INVENTION:
AUDRESSES: ACCENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Geretein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60605-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,611A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 146, Application US/08311611A
Patent No. 5523288
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,401
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,651
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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US-08-311-611A-146
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STATE: Il
COUNTRY:
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APPLICANT: Elsbach, Peter
APPLICANT: Elsbach, Peter
APPLICANT: Elsbach, Deter
TITLE OF INVENTION: Biologically Active
TITLE OF INVENTION: Bactericidal/Permeability-increasing Protein Fragments
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Howard M. Frankfort
STREET: 805 Third Ave.
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                                                                                                                                                                             KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG 120
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                                                                                                               HSNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLF
                                                                                  1 MRENMARGPCNAPRWVSLMVJVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                               Gaps
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  Length 487;
                                               Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMFUTER: IBM PC compatible
COMFUTER: BALENIT Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/173,968
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/754,204
; Score 2507; DB 1;
; Pred. No. 6.6e-209;
0; Mismatches 0;
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYPQTLPVMTKIDSVAGINYGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSNIGPFPVELLQDIMNYIVPILVLPRVNEKLOKGFPLPTPARVQLYNVVLOPHQNFLLF 480
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                                                                                                                                                                                                                                                                                                                               100.0%; Score 2507; DB 1; Length 487; 100.0%; Pred. No. 6.6e-209;
                                                                                                                                                                                                                                                                                                                                                         0; Indels
        CLASSIFICATION: 514
ATTORNEY, AGENT INFORMATION:
NAME: Frankfort, Howard M.
REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5969/05982US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 753-6237
TELEX: 236697
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                              ) ORGANISM: Homo sapiens

TISSUE TYPE: blood

CELL TYPE: promyelocytic leukemia cells

US-08-173-958-2
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Patent No. 5578568
GENERAL INFORMATION:
26-AUG-1991
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Matches 487; Conservative
                                                                                                                                                                                                   MOLECULE TYPE: protein uvporteICAL: YES
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                                                                                                                                                                                                                                              ORIGINAL SOURCE
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William Steve et al. Method of Treating Conditions Associated with Intestinal Ischemia/Reperfusion

APPLICANT: Ammons, TITLE OF INVENTION: TITLE OF INVENTION:

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121 KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180
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                                         3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,527
FLING DATE:
CLASSIFICATION S30
ATTONENT/AGENT INFORMATION:
NAME: SIALPY OF FIRE 31,879
REGISTRATION NUMBER: 31,879
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
TELEPRAK: 312/474-6300
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100.0%; Pred. No. 6.6e-209;
iive 0; Mismatches 0;
                                                                  STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: 111inois COUNTRY: United States of America IP: 60606-6402
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 487; Conservative
                 CORRESPONDENCE ADDRESS: ADDRESSE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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SEQUENCES:
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361 PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
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                                                             301 YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                          VAPPATTAETLDVQMKGEFYSENHHNPPPFFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 146, Application US/08372783
| Patent No. 5578572
| GENERAL INPORMATION:
| APPLICANT: Horwitz, Arnold H.
| APPLICANT: Little, Roger G.
| TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and TITLE OF INVENTION: Materials NUMBER OF SEQUENCES: 237
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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COUNTRY: USA
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
"OWDITER: IBM PC compatible
"TWENTER: TRA PC COMPATIBLE
"TWENTER: TO-DOS/MS-DOS
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APPLICATION NUMBER: 08/273,540
FILING DATE: 11-7UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: RID-LAUGES, Li-HSIEN
REGISTRATION NUMBER: 33,547
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STATE: Illinois
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US-08-372-783-146
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                                                     Sequence 69, Application US/08372783
Sequence 69, Application US/08372783
Patent No. 5578572
GENERAL INFORMATION:
APPLICANT: Lambert, Lewis H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Anti-dram-Positive Bacterial Methods and TITLE OF INVENTION: Materials
NUMBER OF SEQUENCES: 237
CORRESPONDENCE ADDRESS:
ADDRESSEE: Material, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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APPLICATION NUMBER: US/08/372,783
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100.0%; Pred. No. 6.6e-209;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFREENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
PILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-372-783-69
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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487; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                              USA
                     RESULT 10
US-08-372-783-69
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Best Local Si
Matches 487;
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121 KWKAQKRFLKMSGNPDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180
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100.0%; Pred. No. 6.6e-209;
ive 0; Mismatches 0;
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: RID-Laures, Li-Haien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELEPHONE: 312/474-049
TELEPAX: 312/474-046
INFORMATION FOR SEQ ID NO: 69:
REGURE CHARACTERISTICS:
LEGENTH: 25-3856
INFORMATION FOR SEQ ID NO: 69:
REQUENCE CHARACTERISTICS:
LEGENTH: 26-3856
INFORMATION FOR SEQ ID NO: 69:
REQUENCE CHARACTERISTICS:
LEGENTH: 26-3856
INFORMATION FOR SEQ ID NO: 69:
REQUENCE CHARACTERISTICS:
LEGENTH: 26-3856
INFORMATION FOR SEQ ID NO: 69:
REQUENCE CHARACTERISTICS:
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Patent No. S673153
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
APPLICANT: Lim, Edward
APPLICANT: Lambert, Lewis H.
APPLICANT: Scannon, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: "rBPI"
US-08-372-105-69
                                                                                                                                                                                                                                                                                                   LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
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Matches 487; Conservative
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US-08-372-105-146
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                                                                                                                                  KVGWLIQLFHKKIBSALRNRMNSQVCEKVTNSVSSKLQPYFQTLFVMTKIDSVAGINYGL
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                                                                                                              1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                                                       Gaps
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0
                            Length 487;
                                                                   0; Indels
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Sequence 69, Application US/08372105
Sequence 69, Se27153
GENERAL INFORMATION:
APPLICANT: Lim, Edward
APPLICANT: Lambert, Lewig H.
APPLICANT: Lambert, Lewig H.
APPLICANT: Cannon, Patrick J.
TITLE OF INVENTION: Anti-Fungal Materials and Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & BO?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
CONTRY: United States of America
CONTRY: United States of America
ZIP: 66066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,105
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South Wacker Drive
                            100.0%; Score 2507; DB 1; 100.0%; Pred. No. 6.6e-209;
                                                                     0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
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6300 Sears Tower, 233
                                               Best Local Similarity 100.
Matches 487; Conservative
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                            Query Match
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APPLICANT: Little, Roger G. II
APPLICANT: Gazzano-Santoro, Helene
APPLICANT: Parent, James Brian
TITLE OF INVENTION: Therapeutic uses of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Products
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                     KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG 120
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100.0%; Score 2507; DB 1;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/030,644
FILING DATE: 12-MAR-193
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 31580
TELECHONE: 312/474-6300
TELEPHONE: 312/474-6300
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/093,202
                                                                                                                                                                                                                                                       US-08-415-158-2
; Sequence 2. Application US/08415158
; Patent No. 5639727
; GENERAL INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
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STATE: Illinois
COUNTRY: USA
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Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0
                     NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
TITLE OF INVENTION: Anti-Fungal Materials and Methods
NUMBER OF SEQUENCES: 227
                                                                                      STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois CUDYTKY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: F)Oppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-DOS SOUTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                 PILLING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUBER: 08/23,540
FILING DATE: 11-JUL-1994.
PRIOR APPLICATION NUBER: 08/20,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUBER: 08/20,762
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RILL-LAURE, LI-HSIGH
REGISTRATION NUMBER: 33,547
TELEFRONDUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
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                              181 KVGWLIQLFHKKIESALRNKAASQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL 240
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                                                                                          VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV 300
                                                                                                                                                        YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                                                                                                                                                      PIGLIFYPAVDVQAFAVLDPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
                                                                                                                                                                                                                                                                                  YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08064693

Patent No. 5643570

GENERAL INFORMATION

APPLICANT: Theofan, Georgia

APPLICANT: Grinna, Lynn S

APPLICANT: Horwitz, Arnold

TITLE OF INVENTIONS: BPI-Immunoglobulin Fusion Proteins

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,693
FLING DATE: 19930519
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MGYGNET THORNER: 36,989
REGISTRATION NUMBER: 36,989
REGISTRATION NUMBER: 36,989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: AMINO ACID
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Best Local Similarity 100.
Matches 487; Conservative
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STREET: 6300 Sears
CITY: Chicago
STATE: Illlinois
COUNTRY: USA
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US-08-064-693-2
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                                                                      61 KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG 120
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              9
                                                                                                                                                                                                              KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG
                                                                                                                         121 KWKAOKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                                                                                                              KVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

 protein search, using sw model OM protein October 21, 2005, 11:22:38 ; Search time 64.4411 Seconds (without alignments) 1104.324 Million cell updates/sec Run on:

US-10-629-516-2_COPY_10_193 943 1 CNAPRWYSLMYLVAIGTAVT.........HVHISKSKVGWLIQLFHKKI 184 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched: 2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* 1: genesegp19Ana.* Database :

geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aar88746 rBPI(1-19	Aaw16801 Recombina	Aaw16800 Recombina	Aaw47091 Human rec	Aar33777 BPIP from	Aaw16803 Recombina	Aaw16802 Recombina	Aaw62410 Bacterici	Aar21840 Human 57k	Aar71291 Human bac	Aab66058 Human Bac	Abo32712 Secreted	Abu04504 Human exp	Abu04575 Human exp	Adq10386 Human pol	Adq98258 Human pol	Aau06198 Human bac	Aar24777 Sequence	Aar44420 pING4512	Aar43886 Human bac	Aar62370 Recombina	Aar57901 Bacterici	Aar62344 Recombina	Aar68923 Bacterici	Aar71290 Human bac
SUMMARIES	ID	AAR88746	AAW16801	AAW16800	AAW47091	AAR33777	AAW16803	AAW16802	AAW62410	AAR21840	AAR71291	AAB66058	AB032712	ABU04504	ABU04575	ADQ10386	ADQ98258	AAU06198	AAR24777	AAR44420	AAR43886	AAR62370	AAR57901	AAR62344	AAR68923	AAR71290
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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	Recombina	Bacterici	Recombina	Bacterici	Bacterici	Holoprote	rBPI for	Recombina	Recombina	Recombina	Recombina	Recombina	Recombina	Human bac	Bacterici	Human bac	Human bac	Human bac	Human bac	Human rec	
	Aar79185	Aar79021	Aar81247	Aar81245	Aar80995	Aar67998	Aar86455	Aar76243	Aaw05852	Aaw16796	Aaw16816	Aaw16797	Aaw16798	Aar97568	Aaw17987	Aaw44650	Aaw01702	Aaw17986	Aaw47090	Aaw40141	
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	AAR79185	AAR79021	AAR81247	AAR81245	AAR80995	AAR67998	AAR86455	AAR76243	AAW05852	AAW16796	AAW16816	AAW16797	AAW16798	AAR97568	AAW17987	AAW44650	AAW01702	AAW17986	AAW47090	AAW40141	
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	943	943	943	943	943	943	943	943	943	943	943	943	943	943	943	943	943	943	943	943	
	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

bactericidal-permeability increasing protein; BPI; truncated; dimer; endotoxic shock; heparin neutralisation; angiogenesis; inhibitor; ss the native signal 1. .27
| Jabel= signal | Amino acids of the native signal | /note= "the first 4 amino acids of the native signal peptide have been deleted" | Jabel= 220 | /label= rEPI(1-193) | /note= "the first 193 residues of human mature BPI" rBPI(1-193) with 27 amino acid signal peptide. Location/Qualifiers AAR88746 standard; protein; 220 AA 10-APR-1996 (first entry) US5447913-A. Synthetic. AAR88746; Key Peptide Protein AAR88746 ####

94US-00212132. 11-MAR-1994; 05-SEP-1995.

Little RG; (XOMA) XOMA CORP. Ammons WS,

94US-00212132.

11-MAR-1994;

Improved use of a bactericidal-permeability increasing protein - for neutralisation of heparin and treatment of endo-toxaemia, by admin. as covalently linked dimer of N-terminal fragment. WPI; 1995-319904/41.

Example 1; Page ?; 36pp; English.

ų Compositions of N-terminal fragments (i.e. amino acids 1-193 to 1-199) human bactericidal-permeability increasing (BPI) protein are used to neutralise heparin and to treat endotoxaemia. Efficacy of such compsns: is improved when they comprise at least 50% of the truncated rBPI in

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dimeric form. The present sequence is that of rBPI(1-193) in which the first 4 amino acids of the BPI signal peptide are removed, the codon specifying the fifth amino acid of the signal sequence (Met at position - 27) is placed in the context of a consensus Kozak translation initiation sequence. This truncated rBPI is the preferred monomer for dimerisation in the presence of copper 2+ ions. N.B. The patent specification includes the known full-langth BPI sequence but does not contain sequences for any of the truncated versions of the protein. The present sequence has been obtained by modifying the wild-type sequence according to the description given by the inventors
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Sequence 220 AA;

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DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 125
                                                                                                                                                                                                                                  185
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                                                                                                                                                                                                 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
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                                                                                       CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                    KASGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                  Gaps
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 Length 220;
                                0; Indels
100.0%; Score 943; DB 2; 100.0%; Pred. No. 1.4e-92;
                                0; Mismatches
                 Best Local Similarity 100.
Matches 184; Conservative
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AAW16801 standard; protein; 221 AA. (first entry) 28-JUL-1997 AAW16801;

Recombinant endotoxin neutralising polypeptide Lot #159699.

lipopolygaccharide, LPS; bactericidal; permeability; increase; BPI; detection; Gram-negative; bacterium; infection; prevention; treatment; disorder; mediation; stimulation; neutrophil; mononuclear cell; inhibition; shock; anemia; anaemia; disseminated intravascular coagulation; thrombocytopenia; thrombocytopaenia; adult respiratory distress syndrome; ARDS; renal fallure; liver disease; half life; human. Recombinant; endotoxin; neutralisation; RENP; Lot #159699;

sapiens Synthetic. Ношо

Location/Qualifiers 1. .31 /label= sig_peptide Peptide

WO9634873-A1

96WO-US006134 01-MAY-1996; 95US-00431517 01-MAY-1995;

(INCY-) INCYTE PHARM INC.

Marra MN; Scott RW,

WPI; 1996-506090/50.

WO9634873-A1

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The present sequence is the recombinant endotoxin neutralising
polypeptide (RENP) B(1-190) (Lot #15969), which comprises residues 1-190
cf human bactericidal/permeability increasing protein (NBPI). The RENP,
which selectively and specifically binds lipopolysaccharide (LPG) and has
endotoxin neutralising activity, can be used to detect a site of Gram
comparive bacterial infection, and prevent or treat endotoxin related
disorders, preferably where LPS mediated stimulation of neutrophils and
monouclear cells is inhibited, e.g. shock, disseminated intravascular
coagulation, anaemia, thrombocytopaenia, adult respiratory distress
syndrome, renal failure, liver disease and conditions associated with
Gram negative bacterial infection. The RENP has an enhanced serum half
life relative to naturally occurring BPI, and binds LPS without
triggering a significant, undesirable immune response. N.B. Sequence not
given in specification, but produced using the wild type hBPI sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69
            Lipo:polysaccharide binding and endotoxin neutralising polypeptide - useful in diagnosis, prevention and treatment of Gram-negative bacterial infection and associated disorders and conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
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100.0%; Score 943; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.4e-92;
Matches 184; Conservative 0; Mismatches 0;
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/label= sig_peptide
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                                                                                                    Example 1; Page; 147pp; English
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Synthetic.
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                                                                                                                                                                                            The present sequence is the recombinant endotoxin neutralising polypeptide (RENP) B(1-199) (NCY108), which comprises residues 1-199 of human bactericidal/permeability increasing protein (HBPI). THE RENP, which selectively and specifically binds lipopolysaccharide (LPS) and has endotoxin neutralising activity, can be used to detect a site of Gram negative bacterial infection, and prevent or treat endotoxin related disorders, preferably where LPS mediated stimulation of neutrophils and monounclear cells is inhibited, e.g. shock, disseminated intravascular coagulation, anaemia, thrombocytopaenia, adult respiratory distress coagulation, anaemia, thrombocytopaenia, adult respiratory distress cyndrome, renal failure, liver disease and conditions associated with Gram negative bacterial infection. The RENP has an enhanced serum half it erlative to naturally occurring BPI, and binds LPS without given in specification, but produced using the wild type hBPI sequence not given in figure 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                              Lipo:polysaccharide binding and endotoxin neutralising polypeptide - useful in diagnosis, prevention and treatment of Gram-negative bacterial infection and associated disorders and conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bactericidal/permeability increasing protein; BPI; clot formation; TA; clot dissolution; thrombosis; thrombolytic agent; recombinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                 Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 943; DB 2;
100.0%; Pred. No. 1.5e-92;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human recombinant BPI (rBPI23) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW47091 standard; protein; 230 AA.
                                                                                                                                                                            Example 1; Page; 147pp; English
                                            95US-00431517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 184; Conservative
                                                                 (INCY-) INCYTE PHARM INC
                                                                                      Marra MN;
                                                                                                           WPI; 1996-506090/50.
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKKI 184
                                                                                                                                                                                                                                                                                                                                                                             Sequence 230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                                            01-MAY-1995;
 07-NOV-1996
                                                                                       Scott RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW47091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW47091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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This is a recombinant bactericidal/permeability-increasing (BPI) protein product rBPI23. A BPI protein product can be administered especially by contacting with blood to delay or prevent clot formation in the blood or to enhance clot dissolution in the blood. A BPI protein product can also be administered, optionally with a thrombolytic agent (TA), to treat a patient sufferring from thrombotic disorders such as arterial thrombosis, cronary artery thrombosis, etroke, intracardiac thrombosis, peripheral artery thrombosis associated with exposure of blood to a foreign or injured thrombosis associated with exposure of blood to a foreign or injured thrombosis associated with exposure of blood to a foreign or injured tissue surface, hypercoagulability, non-endotoxin-associated coagulopathies, and non-endotoxin-associated disseminated intravascular coagulopathy: The BPI protein products can be used in a method for captulopathy. The BPI protein products can be used in a method for captulopathy are protein products can be used in a method for captulopathy are encorquision in a subject treated with a reperfusion or to reducing recoclusion in a subject treated with a reperfusion or to reducing recoclusion in a subject treated with captured for decreasing the dose of a TA required to establish reperfusion or to reduce reocclusion in a subject comprising co-administration of the BPI protein product and a TA, the dosage of the TA being less than that required for a desired pharmaceutical effect when the TA is administered as a monotherapy. The BPI protein product and a TA transplatic and therapeutic treatment of thrombotic agent captured, thereby reducing or eliminating potential side effects. The subject thereby reducing or eliminating potential side effects. Note: This sequence is not provided in the specification. It has been created benefit encortification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of bactericidal/permeability-increasing protein products - for slowing clot formation and enhancing clot dissolution in blood, particularly for treating thrombotic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                     /note= "mature recombinant rBP123 protein"
                                                                                                                                                                                                                                                                  /note= "wild-type Lys is replaced by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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100.0%; Pred. No. 1.5e-92;
ive 0; Mismatches 0;
                                            1. .31
/note= "signal sequence"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page; 56pp; English
                                                                                                                                                                                                                              /label= K216E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US008017.
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                                                                                                                 32. .230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White ML, Ammons WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-008579/01.
                                                                                                                                                                                         Misc-difference 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV13962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                   WO9742967-A1
                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1997.
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DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120

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inhibitor; endotoxin-felated shock; disseminated intravascular coagulation; anaemia; thrombocytopenia; ARDS; renal failure; endotoxemia; adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The human bactericidal/permeability increasing protein may be used in a compsn. solubilised in a lipid carrier. The BPIP binds lipopolysaccharides and inhibits the immunostimulatory and toxic activities of LPS in vitro and in vivo. The lipid copmsn. stably maintains the BPIP in a sol. active form. The compsn. can be used for cetecting or quantifying LPS in a sample, coating a surgical tool, coating an implantable invasive device, decontaminating a fluid conty. LPC and treating endotoxin related -shock, -disseminated intravascular coagulation, -anaemia, -thrombocytopenia, -adult respiratory stress syndrome or -renal failure, or for preventing endotoxaemia. See also AAR33776, AAR33729-31. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                 Sacterial/permeability increasing protein; lipopolysaccharide; LPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compans. contg. a bactericidal and permeability increasing protein solubilised in a lipid carrier to maintain stably an active form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 943; DB 2; Length 243; 100.0%; Pred. No. 1.6e-92; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilde CG
                                                                                                                                                                                                                                                                                                                                                                                1. .32
/note= "signal peptide"
32. .243
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                         AAR33777 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 7; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snable JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-US008234
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                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scott RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-117241/14.
                                          HKKI 184
                                                                 HKKI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 243 AA;
                                                                                                                                                                                                                                        BPIP from p212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1992;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9305797-A1
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                                                                                                                                                                                              25-MAR-2003
22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra MN,
                                                                                                                                                                    AAR33777;
              130
                                                                    190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                          181
                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                              RESULT
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The present sequence is the recombinant endotoxin neutralising polypeptide (RENP) B(1-212) (Lot #159693), which comprises residues 1-212 of human bactericidal/permeability increasing protein (HBPI). The RENP, which selectively and specifically binds lipopolysaccharide (LPS) and has endotoxin neutralising activity, can be used to detect a site of Gram negative bacterial infection, and prevent or treat endotoxin related disorders, preferably where LPS mediated stimulation of neutrophils and mononuclear cells is inhibited, e.g. shock, disseminated intravascular coagulation, anaemia, thrombocytopaenia, adult respiratory distress syndrome, renal failure, liver disease and conditions associated with Gram negative bacterial infection. The RENP has an enhanced serum half life relative to naturally occurring BPI, and binds LPS without triggering a significant, undesirable immune response. N.B. Sequence not given in specification, but produced using the wild type hBPI sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipo:polysaccharide binding and endotoxin neutralising polypeptide - useful in diagnosis, prevention and treatment of Gram-negative bacterial infection and associated disorders and conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant; endotoxin; neutralisation; RENP; Lot #159693; lipopolysacharide; LFS; bacteritoidal; permeablilty; increase; BPI; detection; Gram-negative; bacterium; infection; prevention; treatment; disorder; mediation; etimulation; neutrophil; mononuclear cell;
70 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
                                                                                130 KWSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKSKVGWLIQLF
                                                         121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibition; shock; anemia; anaemia;
disseminated intravascular coagulation; thrombocytopenia;
thrombocytopaenia; adult respiratory distress syndrome; ARDS;
renal failure; liver disesse; half life; human.
                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant endotoxin neutralising polypeptide Lot #159693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .31
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                       AAW16803 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scott RW, Marra MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-506090/50.
                                                                                                                                         HKKI 184
                                                                                                                                                                                 HKKI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                             AAW16803;
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Gaps

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Conservative

184;

Similarity

Local

Best Loca Matches

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CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQCTAALQKELKRIKIPDYS 1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS

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Example 1; Fig 4; 46pp; English.
                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                     HKKI 184
                                                                                                                               Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                        190 HKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1998
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                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                         AAW62410;
                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the recombinant endotoxin neutralising polypeptide (RENP) B(1-236) (Lot #159695), which comprises residues 1-236
                                                                                                                        DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipo:polysaccharide binding and endotoxin neutralising polypeptide - useful in diagnosis, prevention and treatment of Gram-negative bacterial infection and associated disorders and conditions.
                                                                         9
                                                                                          10 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69
                                                                                                                                                                                                                                                                                                                                 Recombinant; endotoxin; neutralisation; RENP; Lot #159695;
lipopolysaccharide; LPS; bactericidal; permeablilty; increase; BDI;
detection; Gram-negative; bacterium; infection; prevention; treatment;
disorder; mediation; stimulation; neutrophil; mononuclear cell;
                                                                        CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                  KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLP
                                                       Gaps
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                      inhibition; shock; anemia; anaemia;
disseminated intravascular coagulation; thrombocytopenia;
thrombocytopaenia; adult respiratory distress syndrome; ARDS;
renal failure; liver disease; half life; human.
                                    Length 243;
                                                                                                                                                                                                                                                                                                               Recombinant endotoxin neutralising polypeptide Lot #159695.
                                                       Indels
                                                       0
                                    100.0%; Score 943; DB 2;
100.0%; Pred. No. 1.6e-92;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .31
/label= sig_peptide
                                                                                                                                                                                                                                                          AAW16802 standard; protein; 267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page; 147pp; English.
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                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHARM INC.
                                              al Similarity 100.
184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra MN;
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given in figure 3
                                                                                                                                                                                                          HKKI 193
                                                                                                                                                                                         HKKI 184
                    Sequence 243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9634873-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1995;
                                                                                                                                                                                                                                                                                               28-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scott RW,
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                                                                                                                                                                                                                                                                            AAW16802;
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                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                         Matches
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of human bactericidal/permeability increasing protein (hBPI). The RENP, which selectively and specifically binds lipopolysaccharide (LPS) and has endotoxin neutralising activity, can be used to detect a site of Gram negative bacterial infection, and prevent or treat endotoxin related disorders, preferably where LPS mediated stimulation of neutrophils and mononuclear cells is inhibited, e.g. shock, disseminated intravascular coagulation, anaemia, thrombocytopaenia, adult respiratory distress syndrome, renal failure, liver disease and conditions associated with Gram negative bacterial infection. The RENP has an enhanced serum half life relative to naturally occurring BPI, and binds LPS without triggering a significant, undesirable immune response. N.B. Sequence not given in specification, but produced using the wild type hBPI sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bactericidal and endotoxin-neutralising peptides - used in treating e.g.
Pseudomonas species infection and in protectively coating prosthetic
devices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bactericidal, Pseudomonas sp, endotoxin shock, bacterial infection, bactericidal permeability increasing factor, B/PI; neutralising; human neutrophil granule bactericidal protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 943; DB 2;
100.0%; Pred. No. 1.8e-92;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bactericidal permeability increasing factor #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW62410 standard; protein; 300 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 184; Conservative
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N-PSDB; AAV39860.
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New recombinant BPI protein - specifically binds to and inhibits endotoxin lethality, for prevention, treatment and diagnosis of endotoxaemia and endotoxic shock.
                                                                      Disclosure; Fig 13; 108pp; English.
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                      Pseudomonas species; (b) with endotoxin neutralising activity; (c) with both endotoxin neutralising activity and bactericidal activity for beudomonas aeruginosa; (d) a hybrid peptide with endotoxin neutralising activity for activity and bactericidal activity, the peptide with endotoxin neutralising activity combined with at least 1 different amino acid sequence of a peptide with endotoxin neutralising activity combined with at least 1 different amino acid sequence of a peptide that has bactericidal activity; and (e) a prosthetic device which has a sufficient amount of BP attached to the surface to inhibit bacterial growth. The peptides of the invention are used in treating bacterial infection such as Pseudomonas strains e.g. for P. aeruginosa at 10-7 to 10-9 M, and Escherichia coli: The peptides are also used to treat endotoxin shock. The present sequence represents bactericidal permeability increasing factor from an example of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                  DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KASGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 189
                                                                                                                                                                                                                                                                                                                                                                                 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 57kd protein p337 which binds to the outer membrane of susceptible
                                                                                                                                                                                                                                                                                                                                           CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                        CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                           Gaps
                The present invention describes bactericidal peptides (BP): (a) for
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                                                                                                                                                                                                                                                             Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endotoxin binding protein; diagnosis, therapy; endotoxemia; endotoxic shock.
                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                             100.0%; Score 943; DB 2; 100.0%; Pred. No. 2.1e-92;
                                                                                                                                                                                                                                                                                           Mismatches
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/label= residues -31
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91US-00681551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gram negative bacteria (BPI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 184; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKKI 193
                                                                                                                                                                                                                                  Sequence 300 AA;
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Region
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WPI; 1992-096879/12

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The BPI binds endotoxin in the presence of serum and plasma and, unlike other known endotoxin binding proteins such as LBP (lipopolysaccharide binding protein), BPI inhibits the immunostimulatory and toxic activities of endotoxin both in vitro and in vivo. Thus BPI can be used in the diagnosis and therapeutic and prophylactic treatment of endotoxin-related disorders including endotoxemia and endotoxic shock
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                                                                                                                                                                                                                                                                                                      DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
                                                                                                                                                                                                                                                                                                                                                                                                 130 KWSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                                                                                                                                                                                 1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                   10 CNAPRHYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                           KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-glycosylated bactericidal-permeability increasing protein prodn. ·
culturing transformed Gram-negative bacteria, useful as antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bactericidal-permeability increasing protein p337 variant.
                                                                                                                                                                                               .;
0
                                                                                                                                                              Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibiotic; permeability increasing protein; p337 variant; endotoxin binding protein.
                                                                                                                                                                                             Indels
                                                                                                                                                          100.0%; Score 943; DB 2;
100.0%; Pred. No. 2.8e-92;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snable JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR71291 standard; protein; 368 AA.
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(first entry)
                                                                                                                                                                           Best Local Similarity 100.
Matches 184; Conservative
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                                                                                                                           Sequence 368 AA;
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02-SEP-1995
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                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                               189
                                                                                                                                                                                                                                                                                                                   KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
                                                                                                                                                                                                                          69
            permeability increasing protein (see AAR71290), which has antibacterial activity against Gram-negative bacteria, inhibits lipopolysacofaride (LPS) directly, and inhibits LPS- mediated tumor necrosis factor production from mononuclear cells. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                             9
protein is a 38 kDa non-glycosylated variant of human bactericidal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding
                                                                                                                                                                                                                CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                       DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
                                                                                                                                                                                                                                                                       KASGNFDLSIEGASISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                                                                                                                                             CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                 Gaps
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                                                                                                                                   Length 368;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Bactericidal Permeability Increasing, BPI protein.
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                                                                                                                                   Score 943; DB 2;
Pred. No. 2.8e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnes TM;
                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 483 AA
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                                                                                                                                     100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                 Conservative
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                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                HKKI 184
                                                                                                         Sequence 368 AA;
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sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders,
                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myocardial infarction; congestive heart disease; blood platelet disorder; thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
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                                                                                                       neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder. The present sequence is a sequence used in a sequence homology alignment with the TANGO/INTERCEPT
                                                                                                                                                                                                                                                                                                                                                           DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
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hormonal disorder, proliferative disorder; cancer, thyroid disorder;
diabetes, multiple sclerosis, lupus, neurological disorder;
Alzheimer's disease, Parkinson's disease; cardiovascular disorder;
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100.0%; Pred. No. 4.1e-92;
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                                                                                                                                                         sequences of the present invention
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99US-00393996.
99US-00420707.
2000US-00479249.
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2000US-00608452
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                                                                                                                                                                                       Sequence 483 AA;
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24-MAY-2000;
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(BARN/) I
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expressed protein tag; EPT; kinase; phosphatase;

Translational profiling, expressed protein tag, EPT; kinase, phosphatase, protease, protease inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; WHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

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The invention relates to secreted polypeptide-related proteins and nucleic acids (TAMGO and INTERCEPT proteins and nucleic acids). The nucleic acids (TAMGO and INTERCEPT proteins and nucleic acids). The uncleic acids, proteins and antibodies specific to the proteins are useful in screening assays, predictive medicine (e.g. diagnostic assays, prognostic and therapeutic methods. The sequences are used in diagnostic, and therapeutic methods. The sequences are used in diagnosing, preventing or treating proliferative disorders (e.g. multiple solerosis or lupus), neurological disorders (e.g. mlupus), neurological disorders (e.g. Alzheimer's disease or Parkinson's disease), blood placelet disorders (e.g. myocardial infarction or congestive heart disease), blood placelet disorders (e.g. thrombocytopenia or ansemia) and disorders cids may also be used in chromosome mapping, tissue typing and forensic biology, and as surrogate markers. This sequence represents a secreted colypeptide-related protein of the invention. Note: The sequence data for this patent was obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                nucleic acid molecule encoding a secreted protein (e.g. TANGO 202, 50 210 or INTERCEPT 217), useful for diagnosing, preventing or tring disorders such as cancer, diabetes or atherosclerosis, and in
                                                                                                                                                                                       Sharp JD, Kirst SJ, Myers PS, Leiby KR;
SA, Wrighton N, Mackay CR, Goodearl ADJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 483;
                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 28F-28G; 482pp; English.
                                                                                                                                                      GOODEARL A D J
                                                                                                                                                                                                              Mccarthy
KIRST S J.
MYERS P S.
MYERS P S.
LEIBY K R.
HOLTZMAN D A.
MCCARTHY S A.
WRIGHTON N.
                                                                                                                                                                                         Barnes TM,
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                                                                                                                                                                                                                                                                                                                                       forensic biology
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(MCCA/)
(WRIG/)
(MACK/)
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                                                           LEIB/)
                       (KIRS/)
                                      (MYER/)
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Chicz RM, Tomlinson AJ, Urban RG;

(ZYCO-) ZYCOS INC.

20 - FRA - 2001; 20010S - 0292544P. 08-AUG-2001; 2001US - 0310801P. 01-CCT-2001; 2001US - 0336780P. 200-FEB-2002; 2002US - 035895EP.

28-MAR-2002; 2002WO-US009671

28-MAR-2001;

WO200278524-A2 Homo sapiens.

10-OCT-2002

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                                                                                                                                             DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 125
                                                                                                                                                                           KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
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                                                                                      CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                  DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL
                                                           CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                              Gaps
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0
                           0; Indels
100.0%; Score 943; DB 6;
100.0%; Pred. No. 4.1e-92;
iive 0; Mismatches 0;
                            184; Conservative
               Similarity
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Human expressed protein tag (EPT) #1170.

(first entry)

29-JAN-2003

ABU04504;

ABU04504
ID ABUC
XX
AC ABUC
XX
DT 29-3
XX
DE Hume

ABU04504 standard; protein; 483 AA

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fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for receing cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and particularly useful for treating or preventing myeloms, colon cancer, gastric cancer, reating or preventing myeloms or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed grown WIPO at apecification but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
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100.0%; Pred. No. 4.1e-92;
iive 0; Mismatches 0;
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Matches 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                              Translational profiling, expressed protein tag, EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatablity complex; myaloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 943; DB 6; Length 483; 100.0%; Pred. No. 4.1e-92; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                             Human expressed protein tag (EPT) #1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Urban RG;
                                                                                              ABU04575 standard; protein; 483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2001; 2001US-0292544P.
08-MUG-2001; 2001US-0310B01P.
01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0358985P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2002; 2002WO-US009671
                                                                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 184; Conservative
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   186 HKKI 189
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                                                                                                                                                                                                                                                                                                                                                                                                        WO200278524-A2
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2001;
                                                                                                                                                                         29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicz RM,
                                                                                                                                    ABU04575;
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                                                                                ABU045
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The invention relates to human polynucleotides and the polypeptides they encode. The invention also relates to a host cell containing a polynucleotide of the invention, an antibody which selectively binds with a polypeptide of the invention, a method of detecting the presence of a polypeptide in a sample, a method of identifying a compound which binds with a polypeptide, and a method of modulating the activity of a
                                                           180
                 66 DSPKIKHLGKGHYSFYSMDIRBFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 125
                                                                                                                                                                                                                                                                                                                                                                       Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma; anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis; osteoarthritis; arteriosclerosis; hypertension; bacterial infection; psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease; Parkinson's disease; AlDS; tuberculosis; viral infection; malaria; goiter; infertility; endometriosis; muscular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and treating cancer, conscipation, hemorrhoids, cystic fibrosis, hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS, tuberculosis, malaria, goiter, infertility.
                                                                          126 KMSGNPDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                             121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sharp JD, Kirst SJ, Myers PS, Leiby KR; SA, Wrighton N, Mackay CR, Goodearl ADJ;
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                                                                                                                                                                                                                                            ADQ10386 standard; protein; 483 AA.
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27-APR-2000;
24-MAY-2000;
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CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60

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Gaps

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polypeptide. The polynucleotides, polypeptides and compositions are useful for diagnosting, preventing and/or treating cancer, obesity, gastritis, diarrhoea, haemorrhoide, asthma, anaemia, graft-versus-host reactions, allergic reactions, cystic fibrosis, hypogonadism, cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis, hypertension, bacterial infections, psoriasis, diabetes mellitus, hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, AlDS, tuberculosis, viral infections, malaria, goiter, infertility, endometriosis, wounds and muscular disorders. This sequence for this patent did not form part of the printed specification but was sequence uspto.gov/sequence.html.
          88888888888888888888
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Sequence 483 AA;

KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120 CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS Gaps ö Query Match
100.0%; Score 943; DB 8; Length 483;
Best Local Similarity 100.0%; Pred. No. 4.1e-92;
Matches 184; Conservative 0; Mismatches 0; Indels (HKKI 184 61 121 99 181 g ò Бb d ઠે 8 ò

Search completed: October 21, 2005, 11:26:47 Job time : 65.4411 secs

HKKI 189

186

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM\protein

Run on:

October 21, 2005, 11:22:43 ; Search time 37.7407 Seconds (without alignments) 1241.566 Million cell updates/sec

US-10-629-516-2 2507 1 MRENWARGPCNAPRWVSLMV.......NVVLQPHQNFLLFGADVVYK 487 Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	bactericidal/perme	bactericidal perme	bactericidal/perme	lipopolysaccharide	lipopolysaccharide	lipopolysaccharide	lipopolysaccharide	phospholipid trans	plasma phospholipi	hypothetical prote	Φ	cholesteryl ester	cholesteryl ester	probable ligand-bi	probable ligand-bi	hypothetical prote	hypothetical prote	hypothetical prote		hypothetical prote		protein F10D11.6 [hypothetical prote	hypothetical prote	hypothetical prote		I factor protein 2	apolipoprotein B -	hypothetical prote
SUMMARIES		A30909	S10180	S43383	A54136	A35843	156246	843	A53533	149370	C86183	A26941	A53176	146692	S17447	S17448	T29190	T18952	T16889	T20482	T15438	T22700	E87856	T20710	T29001	T30079	T04587	B36186	JH0102	0006
	ΙΩ	A30	S10	S43	A54	A35	156	B3584	A53	I 4 9	088	A26	A53	146	S17	S17	T25	118	116	T20	11	T22	E8.	120	T25	130	T04	B3(Ë	T29
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d	Query Match	100.0	64.9	51.4	43.4	42.0	41.4	39.3	18.5	18.5	13.5	11.8	11.2	10.8	10.4	9.4	8.9	•	7.5	7.4	7.0	6.9	6.1	6.1	5.5	4.9	4.9	4.4	4.3	4.3
	SG	2507	1627.5	1288	1087	1052	1039	985.5	465	463.5	337.5	295	282	271.5	261.5	234.5	222	205.5	189	186.5	175	174	154	154	138	122.5	122	110	109	108
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hypothetical prote probable receptor- cholesteryl ester	receptor protein k bud emergence prot genome polyprotein	glycyl-tRNA synthe probable disease r	nypounelical plote probable peptide s translation initia	apolipoprotein B-1 D-alanine activati	carbamoyl transfer conserved hypothet	hypothetical prote
A97415 H84632 A38700	T50851 A49960 GNVSTV	C83821 H96510	B84683 T50176 H97801	JH0101 E86782	G75093 H81654	T20721
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105 104.5 104	104	103	102.5 101.5 101	100.5	100	100
331		36	3 8 4 0 8	41	4 4 4	45

ALIGNMENTS

N; Alternate names: 55K bactericidal protein
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Accession: A33850; B54136; A29464; A43600; A497166; A30909;
R; Gray, P.W.; Flaggs, G.; Leong, S.R.; Gumina, R.J.; Wēlisē; J.; Ooi, C.E.; Elsbach, P. A; Title: Chem. 264, 9505-9509; 1989
A; Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and A; Reference number: A33850; MUID:89255455; PMID:2722846 bactericidal/permeability-increasing protein precursor - human A; Accession: A33850 A30909

A; Molecule type: mRNA
A; Residues: 1-487 < GRA>
A; Residues: 1-487 < GRA>
A; Residues: 1-487 < GRA>
A; Cross-references: UnFROT: Q9UCT4; GB: J04739; NID: g179528; PIDN: AAA51841.1; PID: g179529
A; Cross-references: University McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon
J. Biol. Chem. 269, 17411-17416, 1994
A; Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-bindi
A; Reference number: A54136; MUID: 94292492; PMID: 7517398

A)Accession: B54136 A)Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA

A.Residues: 1-374, "L', 376-487 «WIL»
A.Residues: 1-374, "L', 376-487 «WIL»
A.Roperimental source: HL-60 cells
A.Note: sequence extracted from NCBI backbone (NCBIP:149855)
R.Sol, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.
R.Oi, C.B.; Weiss, J. 4891-1494, 1987
A.Fitle: A. 25-kDa amino-terminal fragment carries all the antibacterial activities of th A;Reference number: A29464; MUID:88033057; PMID:3667613

A, Accession: A29444
A, Molecule type: protein
A, Residues: 32-51 <001>
A, Experimental source: neutrophils
R, Wasiluk, K.R.; Skubitz, K.M.; Gray, B.H.
A, Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar A, Reference number: A43600; MUID:92040097; PMID:1937776

A; Accession: A43600 A; Molecule type: protein A; Residues: 32-52, R' < WAS> R; Little, R.G.; Kelner, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J. J. Biol. (Chem. 269, 1865-1872, 1994 J. Biol. (Chem. 269, 1865-1872, 1994 A; Title: Functional domains of recombinant bactericidal/permeability increasing protein A; Reference number: A49716; MUID:94124531; PMID:8294435

A,Accession: A49716
A,Molecule type: protein
A,Rolecule type: protein
A,Residues: 32-130;132-141;143-165;202-215,'E',217-225 <LIT>
C,Comment: The bactericidal/permeablity-increasing protein (BPI) is a 60 kD membrane-as which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysaccha between BPI and an LPS-binding protein from liver and cholesteryl ester transfer proteir

Genetics;

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bactericidal/permeability-increasing protein - synthetic (Species: synthetic (Species: synthetic A.Note: Homo sapiens (man) gene engineered and expressed in Bscherichia coli A.Note: Homo sapiens (man) gene engineered and expressed in Bscherichia coli (Jacession: S4333)
R;Qi, S.Y.; Li, Y.; O'Connor, C.D.
Biochem. J. 298, 711-718, 1394
A;Title: The region around residue 115 of human bactericidal/permeability-increasing of a gene coding for the active domain and characterization of recombinant proteins.
                                                                                                                                                                                                                                                                                                                                             GVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVSSKLQPYFOTL-PVMTKIDSVAGINYGLVA-PPATTAETLDVQMKGEFYSENHHNPPPFA
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60 IPNFSGNFKIKYLGKGQYSFFSWVIQGFNLPNSQIRPLPDKGLDLSIRDASIKIRGKWKA
                                                                                                                                                                                                                      300 GALNLTLRDDMIPKESKFRLTTKFFGILIPQVAKMFPDMQMQLFIWASLPPKLTMKPSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGW
                                                                                                                                                 LIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPP
                                                                                                                                                                                                                                                                        245 ATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEA
                                                                                                                                                                                                                                                                                                                                                                                                                   365 TFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                      GPFPVELLQDIMNYIVPILVLPRVNEKLOKGFPLPTPARVQLYNVVLOPHONFLLFGADV
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100.0%; Pred. No. 2e-92;
iive 0; Mismatches 0
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Matches 249; Conserv
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A, Molecule type: DNA
A, Residues: 1-250 <QIS>
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   A;Cross-references: GDB:131572; OMIM:109195
A;Map position: 20q11.23-20q12
C;Superfamily: lipopolysaccharide-binding protein
C;Superfamily: lipopolysaccharide-binding protein
C;Keywords: antibacterial; cytocoxin; glycoprotein; heparin binding; neutrophil
F;1-31/Domain: signal sequence #status predicted <SIG>
F;1-31/Pomain: bactericidal permeability increasing protein #status predicted
F;32-461/Region: bactericidal #status predicted
F;32-51/Region: bactericidal #status predicted
F;380/Binding site: carbohydrate (Asn) (covalent) #status predicted
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S10180

Dactericidal permeability-increasing protein precursor - bovine
C;Species Bos prindgenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10180
R;Leong, S.R.; Camerato, T.
Nucleic Acids Res. 18, 3052, 1990
A;Title: Nucleocide sequence of the bovine bactericidal permeability increasing is A;Accession: S10180
A;Corss-references: UNIPROT:P17453; EMBL:X52563; NID:g138; PIDN:CAA36797.1; PID:(Fill C;Superfamily: lipopolysaccharide-binding protein
F;1-26/Domain: signal sequence #status predicted <S1G>F;27-482/Product: bactericidal permeability increasing protein #status predicted
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                                                                                                                                                                   Query Match 100.0%; Score 2507; DB 2; Length 487; Best Local Similarity 100.0%; Pred. No. 1.4e-186; Matches 487; Conservative 0; Mismatches 0; Indels 0.
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A; Residues: 1-477 <SCH>
A; Residues: 1-477 <SCH>
A; Cross-references: UNIPROT: P18428; GB:M35533; NID:g186965; PIDN: AAA59493.1; PID:g186966 C; Genetics: UNIPROT: P184584 GB: BA; Genetics: BB:LBP
A; Cross-references: GDB: 131571; OMIM: 151990
A; Map position: 20q11.23-20q12
C; Superfamily: lipopolysaccharide-binding protein
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156246
R;Su, G.L.; Freeswick, P.D.; Geller, D.A.; Wang, Q.; Shapiro, R.A.; Wan, Y.H.; Billiar, J. Immunol: 153, 743-752, 1994
A;Title: Molecular cloning, characterization, and tissue distribution of rat lipopolysac A;Reference number: 156246; MUID:94292804; PMID:8021509
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Superfamily: lipopolysaccharide-binding protein
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41.4%; Score 1039; DB 2; Length 4
Best Local Similarity 41.6%; Pred. No. 1.1e-72;
Matches 197; Conservative 109; Mismatches 166; Indels
                                                                                                                                                                                    Query Match
42.0%; Score 1052; DB 2; Length 4
Best Local Similarity 44.1%; Pred. No. 1.1e-73;
Matches 207; Conservative 94; Mismatches 162; Indels
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  A; Molecule type: mRNA
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                                                                                                   Astansiste to a mease to the following protein - human NyAlternate names: LBP; LFS-binding protein - human NyAlternate names: LBP; LFS-binding protein C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: 11-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Species: 11-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Accession: Astanser, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon J. Biol. Chem. 269, 17411-17416, 1994 Procession N.; Snable, J.L.; Lane, J.C.; Leon J. Biol. Chem. 269, 17411-17416, 1994 Procession and lipopolysaccharide (LPS)-binding A; Reference number: Astanser in the compared with conceptual translation A; McCession: Astanser in unclaic acid A; Residues: 1-481 *vML>
A; Cross-references: UNIPROT: P18428
A; Cross-references: UNIPROT: P18428
A; Cross-reference attracted from NCBI backbone (NCBIP:149401)
C; Superfamily: lipopolysaccharide-binding protein
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C;Species: 05-Oct-1990 #sequence_revision 05-Oct-1220 max...__
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1220 max...
C;Accession: A35843
C;Accession: A129-1431, 1990
A;Title: Structure and function of lipopolysaccharide binding protein.
A;Reference number: A35843; MUID:90385281; PMID:2402637
A;Accession: A35843
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 EFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 KESKFRLTTKFFGTFLPEVAKKFPNWKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFAV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 LPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLLELKHSNIGPFPVELLQDIMN 437
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A35843
lipopolysaccharide-binding protein - human
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PPVMEFPAA 250
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C, Accession: A5353

R, Day, J.R.; Albers, J.J.; Lofton-Day, C.E.; Gilbert, T.L.; Ching, A.F.T.; Grant, F.J.; C

J. Biol. Chem. 269, 9388-9391, 1994

A, Title: Complete cDNA encoding human phospholipid transfer protein from human endothelis

A, Reference number: A53533; MUD:94179366; PMID:8132678

A, Recession: A53533

A, Status: preliminary

A, Molecule type: mRNA

A, Residues: 1-493 cDAY

A, Cross-references: UNIPROT:P55058; GB:L26232; NID:9468325; PIDN:AAA36443.1; PID:9468326

C; Genetics: A, Genetics: GDB:340911; OMIM:172425

A, Cross-references: GDB:340911; OMIM:172425

A, Map position: 20pter-20gter

C, Superfamily: lipopolyaeaccharide-binding protein

C, Repwords: Glycoprotein; phosphoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-493/Product: phospholipid transfer protein #status experimental <MAT>
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309 VPADLNIRRTIKSFRPFVPLLANLYPNWNLELQGTVNSEQLVNLSTENLLEEPEMDIEAL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOLDSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RDP-AGRMKVSNVSCQASVSRMHAAFGGTFKKVYDFLSTF---ITSGMRFLLNQQICPVL 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLTT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 ASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELLQDIMNYIVPIL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phospholipid transfer protein precursor - human
NiAlternate names: lipid transfer protein II; PLTP
C.Species: Homo sapiens (man)
C.Species: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
                                                                                                                                                                             369 VVLPSSAREPVFRLGVATNVSATLTLTLTRKITGFLKPGRLQVELKESKVGGFNVELLEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 IPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAF
                                                                                                                                                  376 AVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELLQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGH--YSFYSMDIRE
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                                                                                                                                                                                                                                    436 MNYIVPILVLPRVNEKLOKGFPLPTPARVOLYNVVLOPHONFLLFGADVVYK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                           DB 2; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.5%; Score 465; DB 2; Length 49
Best Local Similarity 26.9%; Pred. No. 4e-28;
Matches 124; Conservative 95; Mismatches 214; Indels
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Lipopolysaccharide-binding protein - rabbit

C; Species: Oryctolagus cuniculus (domestic rabbit)

C; Species: Oryctolagus cuniculus (domestic rabbit)

C; Date: O5-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004

C; Accession: B35843; A46553

R; Schummann, R.R; Leong, S.R; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T

Science 249, 1429-1431, 1990

A; Riccession: B35843

A; Reference number: A35843; MUID:90385281; PMID:2402637

A; Recession: B35843

A; Reference number: A35843; MUID:90385281; PMID:2402637

A; Residues: 1-482 & SCH>
A; Residues: 1-482 & SCH>
A; Residues: 1-482 & SCH>
A; Cross-references: UNIPROT:P17454; GB:M35534; NID:g165467; PIDN:AA899235.1; PID:g165468

A; Rosidues: 1-482 & SCH>
A; Cross-reference number: A46553; MUID:86306528; PMID:2427635

A; Roccession: A46553

A; Molecule type: protein

A; Residues: 2-7-55, XG', 58-62,'P', 64-65 < TOB>
C; Superfamily: lipopolysaccharide-binding protein
C; Keywords: acute phase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDM 315
                                                                                                                                                                                                                     VQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLR 312
                                                                                                                                                                                                                                                DDMLPPDSNIRLNTKAFRPFTPLITRKYPDWNLELLGTVVSAPLLNVSPGNLSLAPQMEI 364
                                                                                                                                                                                                                                                                                                                                                                                            QAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELL 432
                                                                                                                                                                                                                                                                                                                                                                                                                    KIKAVGRGQYEFHSLEIQSCQLRGSSLKPLPGRGLSLSISDSSISVRGKWKVRRSFVKLH 126
                                              GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKK 192
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                                                                                                                                   IESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAETLD
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Matches 193; Conserva
                                                                                      127
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: C86183
A;Accession: C86183
A;Accession: C86183
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                        Similarity
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A; Residues: 1-493 < DRA>
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                                                                                                                                                                                                                                                                            A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                          Best Local Sim:
Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148
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Best Local (
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                                                                                                                             plasma phospholipid transfer protein - mouse
plasma phospholipid transfer protein - mouse
c)species: Mus musculus (house mouse)
c)species: Mus musculus (house mouse)
c)species: Mus musculus (house mouse)
c)Accession: 149370
E;Ablerrs J.J.; Wolfbauer, G.; Cheung, M.C.; Day, J.R.; Ching, A.F.; Lok, S.; Tu, A.Y.
Biochim: Biophys. Acta 1258, 27-34, 1995
A;Title: Functional expression of human and mouse plasma phospholipid transfer protein:
A;Reference number: 149370; MUID:95383401; PMID:7654777
A;Accession: 149370
A;Accession: 149370
A;Accession: UNIPROT: PS5065; EMBL,DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-493 cRES
A;Cross-references: UNIPROT: PS5065; EMBL:U37226; NID:g1051265; PIDN:AAA80542.1; PID:g105
                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPROT:P55065; EMBL:U37226; NID:g1051265; PIDN:AAA80542.1; PID:g109; Superfamily: lipopolysaccharide-binding protein
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T,Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 YPAVDVQ---AFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITASVTITLAPPMLPEVELSKMIMEGRL---SAKLTLRGKALRVKLDLRRFQIYSNQSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 LMVLVAIGTAVTAAVN---PGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHLGKGHYSFYSMDIR--EFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 493;
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              VLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADV
                                      Query Match 18.5%; Score 463.5; DB 2; Best Local Similarity 26.6%; Pred. No. 5.3e-28; Matches 128; Conservative 108; Mismatches 212;
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A;Residues: 1-48 <STO>
A;Gross_references: UNIPROT:Q9MAU5; GB:AE005172; NID:g7211993; PIDN:AAF40464.1; GSPDB:GN
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAPPV-MEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLTTKF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQA---FAVLPNSSLAS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : :|::||:|| : ::
WRFIIPQLYKKYPNQDMNLNISLSSPPLVKISEQ----YVGANVNADLVINVLDANQVIP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 SNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKSDEGGLKLSLSECGCHVEDITIEL-EGGASWFYQGMVNAFKDQIGSSVESTIAKKLTE
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                                                                                                                                                                                                                                                                                            38 VRISOKGLDYASQOGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSS
                                                                                                                                                                                                                                                                                                                                                     31 VLVSQNGLDFVKNLLVNKAIASIIPLQIPRIEKSMKIPFLGGIDVVVSNLTIYELDVASS
                                                                                                                                                                                                                                                                                                                                                                                                                    98 QISMVPNVGLKFSISNANIKISGKWKAQKRF-----LKMSGNFDLSIEGMSISADLKLG
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                   25;
                                                                                                                                                                       13.5%; Score 337.5; DB 2; Length 23.6%; Pred. No. 3.1e-18; ive 87; Mismatches 240; Indels
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F,1-17/Domain: signal sequence #status predicted <SIG>
F,18-493/Product: cholesteryl ester transfer protein #status
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C;Accession: 146692
R;Asgashima, M.; McLean, J.W.; Lawn, R.M.
B;Asgashima, M.; McLean, J.W.; Lawn, R.M.
J. Lipid Res. 29, 1643-1649, 1988
A;Title: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protes
A;Reference number: 146692, MUID:89215620, PMID:3244015
A;Accession: 146692
A;Accession: 146692
A;Status: preliminary; translated from GB/BMBL/DDBJ
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A;Residues: 1-497 <NAG>
A;Cross-references: UNIPROT:P22687; GB:M27486; NID:g530906; PIDN:AAA31199.1; PID:g530907
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                                                                                                                                                                                                                      314
                                                                                                                                                                                                                                                                                                                                                                                                         382 -SLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELLQDIMNYIV 440
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                                209 VINSVSSKLOPYFOTLPVMTKIDSVAGINYGLVAPPATTAETLDVOMKGEFYSENHHNP- 267
                                                                                                                                                                                                                                                                                 326 TKFFGT---FLPBVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFAVLPNS- 381
                                                                                                                                                                                                                                                                                                                                               TWGFNTNOEIFQEVVGGFPS-QAOVTVHCLKMPRISCONKGVVVNSSVMVKFLFPRFDQQ 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholesteryl ester transfer protein - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                            263 PLPTFSPALL----GDSRMLYFWFSEQVFHSLAKVAFQDGRLTLSLMGD----EFKAVLE
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                                                                       --PPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholesteryl ester transfer protein - crab-eating macaque (Species: Macaca fascicularis (crab-eating macaque) (C;Species: Macaca fascicularis (crab-eating macaque) (C;Accesion: A51176 # sequence_revision 12-May-1994 # text_change 07-May-1999 (C;Accession: A51176 # sequence_revision 12-May-1994 # text_change 07-May-1999 (C;Accession: A51176 # sequence_revision 11, 1759-1771, 1991 Arterioscler: Thromb. 11, 1759-1771, 1991 A;Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl same high density lipoprotein levels.

A;Reference number: A53176 # MUD:92031355; PMID:1931878 A;Accession: A53176 # MUD:92031355; PMID:1931878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TASYLESHHKGHPIYKNVSEDLPLPTFSPTLL----GDSRMLYFWFSERVFHSLAKVAFQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 AGVLKMTLRDDMIPKESKFRLTTKFFGT----FLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTGLTFYPAVDVQAFAVLPNS--SLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTVSNLTESSSESIQSFLQSMITAVGIPEVMSRLEVVFTALMNSKGVSLFDIINPEIITR 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSSQISMVPNVGLKFSISNANIKISGKWK---AQKRFLKMSGNFDLSIEGMSISADLKLG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNPT--SGKPTITCSSCSSHINSVHVHI-SKSKVGWLIQLFHKKIESALRNKMNSQVCEK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIDOSIDFEIDS---AIDLOINTOLICDSGRVRTDAPDCYLSFHKLLLHLGGEREPGWIK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKHSNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGF-PLPTPARVQLYNVV---LQPH 474
                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMSGNFDLSIEGMSISADLKLGSNPT--SGKPTITCSSCSSHINSVHVHI-SKSKVGWLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLFHKKI ESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKI DSVAGI NYGLVAPPAT
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                                                                                                                              SLMVLVAIGTAVTAAV----NPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSF
                                                                                                                                                                                                                                                          KIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWK---AQKRFL
                                                                    Gaps
                                                                    38;
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   Length 493;
   11.8%; Score 295; DB 2; Length 493
23.7%; Pred. No. 6.2e-15;
ive 92; Mismatches 243; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233; Indels
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Query Match
Best Local Similarity 23.7
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNFLLFGAD 483
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A; Residues: 1-493 < PAP>
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Best Local S
Matches 111
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                                                                                                                                                                                                                                                                                                                                                   SNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHIN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                              172 SVHVHISKSKVGWLIQLFHKKIESALRNKWNSQVCEKVTNSVSSKLQPYFQTLPVMTKID 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 --HDRMYYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPP---NMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLPPGQHLLLSLRVMKS--PMILLQNKKYTVSIPVTIHVLSSVPQGTPVALFQMNGVMTL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 SMEVSAESNRLVGELKLDRLLLELKHSNIGPPPVELLQDIMNYIVPILVLPRVNEKLQKG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 NAHLVPSTTKLHISLSLERLTVQLASSFSQPFDASRLEEWLSDVVRAAYMQKLNEHLEVG 444
                                                                                                                                                                                         3 PGVYALLLLWGLATPCLGLLETVGTLARIDKDELGKAIQNSLVGGPILQNVLGTVTSVNQ
                                                                                                                                                                                                                                                                                                                                                                                163 TLLGHİSLTS-GLLPTPIFGLVEQTLCKVLPGLLC-PVVDSVLSVVNBLLGATLSLVPLG
                                                                                                                                                              13 PRWVSLMVLVAIGTAVTAAVNP-GVVVRISQKGLDYASQO---GTAALQKELKRIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 SVAGINYGLVAPPATTAETLDVQMKGEFYSENHENP--PPFAPPVMEFPAA-----
              A; Cross-references: EMBL: X60658; NID: 957733; PIDN: CAA43065.1; PID: 957734
                                                                Query Match 9.4%; Score 234.5; DB 2; Best Local Similarity 21.8%; Pred. No. 2.9e-10; Matches 109; Conservative 88; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 FPLPTPARVOLYNVVLQPHQN 476
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A;Residues: 1-473 <DEA>
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                                                                                                                                                                                       RESULT 14
S17447
probable ligand-binding protein RY2G5 - rat (fragment)
C;Species: Rattue norvegicue (Norway rat)
C;Species: Rattue norvegicue (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 22-May-1998 #text_change 05-Nov-1999
C;Accession: 317447
R;Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.
EMBO J. 10, 2813-2819, 1991
A;Title: Novel genes for potential ligand-binding proteins in subregions of the olfactor A;Reference number: $17447
A;Molecule type: mRNA
A;Residues: 1-470 cDEA>
A;Cross-references: EMBL:X60660; NID:g57731; PIDN:CAA43067.1; PID:g57732
A;Cross-references: Difactory mucosa
C;Genetics:
C;Genetics:
A;Gene: RY2G5
C;Keywords: olfaction
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: 817448
R;Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.
A;Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.
A;Title: Novel genes for potential ligand-binding proteins in subregions of the olfactor A;Reference number: 817447; MUD:92007724; PMID:1915264
A;Status: preliminary
A;Molecule type: mRNA
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Fri Oct 21 12:25:53 2005

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 21, 2005, 11:22:43 ; Search time 64.7154 Seconds (without alignments) 1455.954 Million cell updates/sec Run on:

US-10-629-516-2_COPY_10_193 943 1_CNAPRWVSLMVLVAIGTAVT.........HVHISKSKVGWLIQLFHKKI 184 Title: Perfect score: Sequence:

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1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

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SUMMARIES

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# ALIGNMENTS

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EMBL, AL359555, CAC13043.1, --
EMBL, AL499625, CAC1350.1, --
EMBL, AL391692, CAC10453.1, --
PDB, IBNF, X-ray, @=28-483.
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| Drotein. | Cleavage sites for elastase (Potential). | Cleavage sites for elastase (Potential). | V -> A (in dbSNP:1341023). | FTId=VAR 018401. | A -> V (in dbSNP:5743509). | FTId=VAR 018402. | FTId=VAR 018403. | FTId=VAR 018403. | FTId=VAR 018403. | FTID=VAR 018403. | F -> L (in Ref. 2). | F -> L (in Ref. 2). | F -> L (in Ref. 2). | F -> L (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref. 3). | F -> R (in Ref.
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3D-structure; AntibioFic; Direct protein sequencing; Glycoprotein; 3D-structure; AntibioFic; Direct protein sequencing; Glycoprotein; Slgnal; Transmembrane.
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A Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Itschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Branchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                     Score 943; DB 1; Length 4 Pred. No. 3.7e-75; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; RCO40955; AAH40955.1; -.
HSSP; P17213; 1EWF.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Bactericidal/permeability-increasing protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sci. U.S.A. 99:16899-16903(2002)
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0008289; F:lipid binding; IEA.
InterPro; IPR001124; IBP BFI_CETP.
Pfam; PF01273; IBP_BFI_CETP; 1.
Pfam; PF02886; IBP_BFI_CETP_C; 1.
SMART; SM00328; BPT1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Blood;
                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         181 HKKI 184
                                                                                                                                                                                                                                                                                                    186 HKKI 189
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
                                                                   184;
                                                                                                                                                                                                                 121
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                                        Query Match
Best Local
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93 VPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 152
                                                                                                                                                                                                                                                                                                                      61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
                                                                                                                                                                                                                                                                                                                                                     10 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 129
                                                                                                                                                                                                                                                                                                                                                                                                                              121 KMSGNPDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWL1QLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 QKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISM
                                                                                                                                                                                                                                        10 CNAPRWĄSIAWLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QKGLDYASQQGTAALQKELKRIKIPDYSGSFKIKLLGKGRYSFYSMDIREFQLPSSQISM
                                                                                                                                                                                           1 CNAPRWYSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MRR-2001 (TrEMBLrel. 16, Created)
01-MRR-2001 (TrEMBLrel. 16, Last sequence update)
01-MRR-2003 (TrEMBLrel. 25, Last annotation update)
Bactericidal/permeablilty-increasing protein (Fragment).
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus fragment).
Macaca mulatta (Rhesus fragment).
Macaca mulatta (Rhesus fragment).
Creationia; Metheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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88.2%; Pred. No. 5.1e-53;
tive 9; Mismatches 9; Indels
                                                                                                       Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu J., Wang H.;
Xu J., Wang H.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF312587; AAG42843.1;
HSSP; P17213; IEWF.
GO; GO:0003289; F:lipid binding; IEA.
InterPro; IPR001124; IBP BPI_CETP.
Ffan; PF01213; IBP_BPI_CETP;
SMART; SM00328; BPII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 AA; 19772 MW; F1B180A02A38CE63 CRC64;
SMART; SM00329; BPI2; 1.
PROSITE; PS00400; LBP BPI CETP; 1.
SEQUENCE 487 AA; 53880 MW; FE709D9317E5206D CRC64;
                                                                                                       99.6%; Score 939; DB 2;
99.5%; Pred. No. 8.4e-75;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCSSCSSHINSVHVHISKSKVGWLIQLFHKKI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCSSCSSHINSVHVRISNSRVGWLIRLFRKKI 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 134; Conservative
                                                                                                          Query Match
Best Local Similarity 99.5
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HKKI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 HKKI 193
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FKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKM 122

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67 FKIKYLGKGQYSFFSMVIQGFNLPNSQIRPLPDKGLDLSIRDASIKIRGKWKARRNFIKL 126
                                                                                                                            123 SGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHK 182
                                                                                                                                                                                         183 KI 184
                                                                                                                                                                                                                                                                                                                                        O6AXU0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOWAIN: The N-terminal region may be exposed to the interior of the granule, whereas the C-terminal portion may be embedded in the membrane. During phagocytosis and degranulation, proteases may be released and activated and cleave BPI at the junction of the N- and C-terminal portions of the molecule, providing controlled release of the N-terminal antibacterial fragment when bacteria are ingested (By similarity).
                                                                                                                                                                                                                                                                                                                                Leukocytes (PMN) granules (By similarity).
TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage sites for elastase (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.3%; Score 596.5; DB 1; Length 482; 63.2%; Pred. No. 2e-44;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Bactericidal permeability-increasing protein precursor (BPI).
                                                                                                                                                                                                                                                                                               Leong S.R., Camerato T.; "Nucleotide sequence of the bovine bactericidal permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             že-44;
ches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -IIDKEG (GICNAC. . .) (Po
DD7D59AE785BC42D CRC64;
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Antibiotic, Glycoprotein; Membrane, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Fred. NO. 2e-4
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X52563, CAA36797.1; -.
PIR; $10180; $10180.
HSSP; P17213, 1EMF.
InterPro; IPR001124; LBP BPI_CETP.
Pfam; PF01273; LBP_BPI_CETP; 1.
SMART; SM00328; BPII; 1.
SMART; SM00329; BPII; 1.
                                                                                                                                                                                                                                                      TISSUE-Bone marrow;
MEDLINE-90272418; PubMed=2349103;
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303
375
389
                                                                                                          Bos taurus (Bovine).
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303
375
389
463
482 AA;
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Matches 115; Conserv
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
                                                                                                                                                                     Bovinae, Bos.
NCBI_TaxID=9913;
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CARBOHYD
                                                                                       Name=BPI;
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Straubberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zebeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Rhopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Astapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan R.J., Malkan B.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahe J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
An Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.J.,
And Marra M.J., Saalska U., Smailus D.E., Schnerch A., Schein J.E.,
And Marra M.J.,
And Marra M.J., Smailus D.E., Schnerch A., Schein J.E.,
And Manner D.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 AA; 53751 MW; 269591C4C2F5A6D1 CRC64;
                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                        Bactericidal/permeability-increasing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12477932; DOI=10.1073/pnas.242603899;
482 AA.
PRT;
PRELIMINARY;
                                                                                                                                                                                                                                              Rattus norvedicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 109; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
                                                                                                                                                                                                                Name=Bp1;
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62 99

APRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDS

Conservative

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[4]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                 FROM N.A.
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 NCBI_TaxID=10090;
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                   SEQUENCE
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                                                         185
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                                                                                                                                                                                                                                                                                                                                                                                                                                               62 SFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 MSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFH 181
  121
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                                                                                                                                                                                                                                                                                                                                                                                                                       7 NVRKWSALLLLAIIGTALTAATDPGFVAMISQKGLDFACQQGVVELQKELQAISVPDFSG
  SFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLK
                                                 MSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFH
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male epididymis cDNA, RIKEN full-length enriched
library, clone:9230105K17 product:weakly similar to
bactericidal/permeability-increasing protein.
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                     Length 483;
                                                                                                                                                                                                                                                            Bingle C.D., Craven J.;
Bingle C.D., Craven J.;
Bingle C.D., Craven J.;
Bingle C.D., Craven J.;
Bingle C.D., Craven J.;
Bingle C.D., Craven J.;
Bingle C.D., Craven J.;
Interpro; IPR001124; LBP BPI CETP.
Pfam; PF01273; LBP BPI CETP. J.
Pfam; PF02886; LBP BPI CETP. J.
SWART; SM00328; BPI2; I.
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                    483 AA; 53940 MW; 4AA2D48095C52B74 CRC64;
                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Bactericidal/permeability-increasing protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                     58.8%; Score 554.5; DB 2 57.9%; Pred. No. 1.1e-40;
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                                                                                                                                              483 AA
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                                                                                                                                                                 Created)
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                                                                                                                                                                (TrEMBLrel. 28,
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                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=9230105K17Rik;
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Best Local Similarity
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RKI 188
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RKI 188
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                                                                             KKI 184
                                                                                                                                                        Q67E05;
25-OCT-2004
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QBBSF3
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Q67E05
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STRAIN-C57BL/6J; TISSUE=Epididymis;
MEDLINE=20499374; PubMed=11042199; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.":
STRAIN=CS7BL/67; TISSUB-Epididymis; MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=Epididymis; STRAIN=C57BL/6J; TISSUB=Epididymis; STRAIN=C57BL/6J; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Yamamoto R., Mazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watsuhiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RKEN integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                       "Punctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Epididymis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CORSOTTIUM;
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GQ; GQ:00008289; F:11pid binding; IEA
GC; GC:000289; F:11pid binding; IEA
InterPro; IPR001124; IEB BPI CETP.
Pfam; PF01273; IBP_BPI CETP; I.
Pfam; PP02886; IBP_BPI CETP_C; 1.
SWART; SW00328; BPI; I.
SWART; SW00329; BPIZ; I.
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STRAIN=C57BL/6J; TISSUE=Epididymis;
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STRAIN=C57BL/6J; TISSUE=Epididymis;
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HSSP; P17213; 1BP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Length 486;

DB 2;

Score 554.5;

58.8%;

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Eukaryota; Metazoa;
Mammalia; Eutheria;
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CARBOHYD
SEQUENCE
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LBP_MOUSE
ID _ LBP_M
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DT 01-NO
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                                                                                                                 93 VPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 152
                                                                  SFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLK 121
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                                        2 NAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSD
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Bactericidal permeability-increasing protein (BPI) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                              55.0%; Score 518.5; DB 2; Length 178; 62.5%; Pred. No. 5.5e-38; ive 29; Mismatches 27; Indels 1.
           43; Indels
                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Bactericidal/permeability-increasing protein (Fragment)
                                                                                                                                                                                                                                                                                                                                Wang H.;
ed (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          178 AA; 19693 MW; 867D7C6CA14B3A75 CRC64;
 Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCSSCSSNINRARLRVS-GILGWLLKLFHKRI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCSSCSSHINSVHVHISKSKVGWLIQLFHKKI 184
          33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0008289; F:lipid binding; IEA.
InterPro; IPR001124; LBP BPI CETP.
PFdan; PF01273; LBP BPI (ETP; 1.
SMART; SM00328; BPII; I.
                                                                                                                                                                                                                                  Created)
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Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                 EMBL; AF322586; AAG42842.1;
HSSP; P17213; 1BP1.
57.9%;
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           Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                               PRELIMINARY;
  Best Local Similarity
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95; Conserv
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                              KKI 184
                                                                                                                                                                RKI 188
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
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Q28739;
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Submitted
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).

DOMAIN: The N-terminal region may be exposed to the interior of bownin; whereas the C-terminal portion may be embedded in the membrane. During phagocytosis and degranulation, proteases may be released and activated and cleave BPI at the junction of the N-and C-terminal portions of the molecule, providing controlled release of the N-terminal antibacterial fragment when bacteria are ingested (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QKGLDYACQQGVAVLQKELEKIRIPDVSGKFKLRPFGKGHYNFHSLVVRSFQLDNPQIRL
                                                                                                                          SECUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE-Bone marrow;
STRAIN=New Zealand white; TISSUE-Bone marrow;
Weiss J., Weinrauch Y., Levy O., Flynn S.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: The cytotoxic action of BPI is limited to many species of Gram-negative bacteria; this specificity may be explained by a strong affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the Gram-negative bacterial outer envelope (By similarity).
-!- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear Leukocytes (PMN) granules (By similarity).
-!- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 QKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ingested (By similarity).
SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -linked (GlcNAc. .) (Potential) 209AE0894FEDACFC CRC64;
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Chordata, Craniata, Vertebrata, Eu
Lagomorpha, Leporidae, Oryctolagus
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62.5%; Pred. No. 1.8e-36;
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N-linked (GlCNAC.
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PROSITE; PS00400; LBP_BPI_CETP; PARTIAL.
Antibiotic; Glycoprotein; Transmembrane.
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Pfam; PF01273; LBP BPI CETP; 1.
Pfam; PP02866; LBP EPI CETP C; 1.
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Best Local Similarity 62.53
Matches 95; Conservative
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SMART; SM00329; BPI2;
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352
445 AA;
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Altachner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toophyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Kraywinski M.I., Skalaka U., Smallus D.E.,

Butterfield Y.S.N., Kraywinski M.I., Skalaka U., Smallus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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-!- FUNCTION: Binds to the lipid a moiety of bacterial lipopolysaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. The LBP/LPS complex seems to interact with the CD14 receptor.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                               MEDLINE=97289150; PubMed=9144073;
Lengacher S., Jongeneel C.V., le Roy D., Lee J.D., Kravchenko V.,
Ulevitch R.J., Glauser M.P., Heumann D.;
"Reactivity of murine and human recombinant LPS-binding protein (LBP)
within LPS and Gram-negative bacteria.";
J. Inflamm. 47:165-172(1995).
                                              Mus musčulus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1038776; Lbp.
GO:0001530; F:lipopolysaccharide binding; IDA.
InterPro; IPR001124; Lbp BPI_CETP.
Pfam; PF01273; LBP BPI_CETP; 1.
Pfam; PF02886; LBP BPI_CETP. 1.
SMART; SM00329; BPII; 1.
PROSITE; PS00400; LBP BPI_CETP; 1.
Antibiotic; Glycoprotein; Lipid transport; Signal; Transmembrane.
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N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
C -> G (in Ref. 2).
K -> Q (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                               Lipopolysaccharide-binding protein precursor (LBP)
   05-JUL-2004 (Rel. 44, Last annotation update)
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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Ray Etrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., McKwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Rabey J., Halton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Anting M. M. Touchman J.W., Green E.D., Dickson M.C.,
Anting M. I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Annes S.J., Marra M.J.,
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 KIKHLGKGHYSFYSMDIREPQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMS 123
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                                                                                                                                                                                                                                                                                                                                         DB 1; Length 481;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
102 R -> S (in Ref. 2).
280 A -> S (in Ref. 2).
310 H -> P (in Ref. 2).
313 G -> S (in Ref. 2).
341 R -> G (in Ref. 2).
382 S -> G (in Ref. 2).
396 TR -> NS (in Ref. 2).
418 I -> M (in Ref. 2).
53312 MW; 34EA9C066C9AB678 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        3e-31;
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Best Local Similarity 47.0%; Pred. No. 3e-31
Matches 85; Conservative 43; Mismatches
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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sequencing of human lipopolysaccharide-binding protein

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EMBL;
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                                                                                                                                                                                                                                                                                                                                      GRGRYEFHSLNIHSCELLHSALRPVPGQGLSLSISDSSIRVQGRWKVRKSFFKLQGSFDV 131
                                                                                                                                                                                                                                                68
                                                                                                                                                                                                                                                                    MEDLINE=90110577; PubMed=9441745; DOI=10.1006/geno.1997.5030; Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D., Seilhamer J.J., Schumann R.R.; "Similar organization of the lipopolysaccharide-binding protein (LBP) and phospholipid transfer protein (PLTP) genes suggests a common gene family of lipid-binding proteins."; Genomics 46:416-425(1997).
                                                                                                                                                                                                                                              9 LMVLVAIGTAVTAAVNPGVVVRISOKGLDYASOOGTAALOKELKRIKIPDYSDSFKIKHL
                                                                                                                                                                                                                                                                                                                                                                                                         SIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKI 184
                                                                                                                                                                                                            Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94292492; PubMed=7517398; Wilde C.G., Sellhamer J.J., McGrogan M., Ashton N., Snable J.L., Land C.G., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.; Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-binding protein. LPS binding properties and effects on LPS-mediated cell activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90385281; PubMed=2402637; Schumann R.R., Leong S.R., Flaggs G.W., Gray P.W., Wright S.D., Mathison J.C., Tobias P.S., Ulevitch R.J.; Structure and function of lipopolysaccharide binding protein."; Science 249:1429-1431(1990).
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                                                                                                                                                                             Length 477;
                                                                                                                                                                                                            54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hubacek J.A., Aslanidis C., Schmitz G.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
            GO, GO.0008289; F:lipid binding; IEA.
InterPro; IRR001124; LBP_BPI_CETP.
Pfam; PP01273; LBP_BPI_CETP_1.
SMART; SM00328; BPI]; I.
SMART; SM00328; BPI]; I.
PROSTTE; PRO$4009; LBP_BPI_CETP_7.
SMART; SM00329; BPI]; I.
SMORT; SM00329; BPI; I.
SMORT; SM00329; BPI; I.
SMORT; SM00329; BPI; I.
SMORT; PRO$5778; PRO$60400; LBP_BPI_CETP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P18478; 043438; 092672; 094403; 09UD66; 01-NOV-1990 (Rel. 16, Created) (Rel. 27, Last sequence update) 05-UUS-2004 (Rel. 44, Last annotation update) Lipopolysaccharide-binding protein precursor (LBP).
                                                                                                                                                                         ch 45.5%; Score 429; DB 2; Similarity 46.6%; Pred. No. 1.5e-29; B2; Conservative 38; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                  MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
MeDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
Deloukas P., Barles G.H., Bartes M.M., Beare D.M.,
Bailey J., Barlow K.F., Bates K.M., Beare D.M.,
Bailey J., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chap Burrill W.D., Butler A.B., Carder C., Carter N.P.,
Colson A., Coville G.J., Collier R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Grafham D.V., Garffiths M.N.D., Gwilliam R., Hall R.E.,
Hunnend S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Milne S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
A kuce C.D., Smith M.L., Socht C.E., Sehward C.A., Sulston J.E.,
Swann R.M., Sycamore N., Taylor R., Tree L., Thomas D.W., Thorpe A.,
Swann R.M., Sycamore N., Taylor R., Tael M., Thorpe A.,
Mitchead S.L., Mittaker P., Willey D.L., Williams L., Williams S.A.,
Whitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Whitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Whitchead S.L., Whittaker P., Willey D.L., Williams S.A.,
Whitchead S.L., Whittaker P., Willey S.M.,
Whitchead S.L., Whittaker P., Willey S.M.,
Whitchead S.L., Whitley S. Willey S.M.,
Whitchead S.L., Whitley W.W., Hubbard T., Durbin R.M., Bentley D.R., Bentley D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Binds to the lipid a moiety of bacterial lipopolysaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. The LBP/LPS complex seems to interact with the CD14 receptor.

-i- SUBCELULAR LOCATION: Secreted.

-i- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comparative analysis of human chromosome 20.";
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                                          Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 25:469-471(1998)
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MEDILINE-9822782; PubMed-9568897;
Beamer L.J., Carroll S.F., Eisenberg D.;
"The BPI/LBP family of proteins: a structural analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-41 FROM N.A.
Sutton C.L., Smith R.I.F., Centola M.B., Theofan G.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
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EMBL, X98657; CAA67226.1; --
EMBL, X98659; CAA67226.1; JOINED.
EMBL, X98659; CAA67226.1; JOINED.
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X98661; CAA67226.1;
X98662; CAA67226.1;
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CAA67226.1;
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X98668;
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EMBL;
EMBL;
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Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;

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                                         Name=Lbp
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N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
R -> H (in Ref. 2).
E -> C (in Ref. 2).
S -> F (in Ref. 4).
VTAS. -> GYCL (in Ref. 4).
VTAS. -> GYCL (in Ref. 4).
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L -> F (in Ref. 2).
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GO; GO:0005963; P:acute-phase response; TAS.

GO; GO:0005968; P:cellular defense response; TAS.

GO; GO:0005968; P:cellular defense response; TAS.

GO; GO:0009618; P:cellular defense response; TAS.

GO; GO:0009618; P:cellular defense response; TAS.

InterPro; IPR001124; LBP BPI_CETP.

InterPro; IPR001273; LBP BPI_CETP.

SMART; SM00328; BPII; I.

SMART; SM00329; BPII; I.

SMART; PS004400; LBP BPI CETP; 1.

Antibiotic; Glycoprotein; Lipid transport; Signal; Transmembrane.
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                                                    AF013502; AAC39547.1; JOINED.
AF013503; AAC39547.1; JOINED.
AF013504; AAC39547.1; JOINED.
AF013505; AAC39547.1; JOINED.
AF013506; AAC39547.1; JOINED.
AF013507; AAC39547.1; JOINED.
AF013509; AAC39547.1; JOINED.
AF013510; AAC39547.1; JOINED.
AF013511; AAC39547.1; JOINED.
AF013511; AAC39547.1; JOINED.
AF013511; AAC39547.1; JOINED.
AF013511; AAC39547.1; JOINED.
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MIM; 151990; -.
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EMBL, AF013507, AAC3956
EMBL, AF013508, AAC3956
EMBL, AF013509, AAC3956
EMBL, AF013511, AAC3956
EMBL, AF013511, AAC3956
EMBL, AF013511, AAC3956
EMBL, AL080249, CAC1040
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                                         EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
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AC Q63
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                                                                                                                                                                                                                                               STRAINE-Sprague-Dawley; TISSUR-Liver;

MEDLINE-94292804; PubMed-8021509;

MEDLINE-94292804; PubMed-8021509;

Billiar T.R., Freeswick P.D., Geller D.A., Wang O., Shapiro R.A., Wan Y.H.,

Billiar T.R., Tweardy D.J., Simmons R.L., Wang S.C.;

"Molecular cloning, characterization, and tissue distribution of rat lipopolysaccharide binding protein. Evidence for extrahepatic expression.";

J. Immunol. 153,743752 (1994).

I. J. Immunol. 153,743752 (1994).

I. FUNCTION: Binds to the lipid a moiety of bacterial ipopolysaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. The LBP/LPS complex seems to interact with the CD14 receptor.

C. I. SUBMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 KIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus forvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBL TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 481 Lipopolyaaccharide-binding protein. 300 300 N-linked (GlcNAc. .) (Potential). 355 355 N-linked (GlcNAc. .) (Potential). 481 AA; 53600 MW; 23E67CB9CC97D2FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Indels
05-JUL-2004 (Rel. 44, Last annotation update)
Lipopolysaccharide-binding protein precursor (LBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.4%; Score 428; DB 1;
44.2%; Pred. No. 1.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L32132; AAA21835.1; -. PIR; I56246; I56246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80; Conservative
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                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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127 DLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKI 184
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InterPro; IPR001124; LBP BPI_CETP.
Pfam; PF01273; LBP BPI_CETP; 1.
Pfam; PF02886; LBP BPI_CETP_C; 1.
SMART; SM00328; BPII; 1.
SMART; SM00329; BPII; 1.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=90385281; Pubmed=2402637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M35534; AAA99235.1; -. PIR; B35843; B35843.
                                                                                          STANDARD:
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387
57
63
482 AA;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 27-66.
                                                                                                                             01-NOV-1990 (Rel
05-JUL-2004 (Rel
                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                      TISSUE=Serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                          LBP RABIT
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CONFLICT
SEQUENCE
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                                                                              LBP_RABIT
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    à
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Astapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toophyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garria A.M., Gasy L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Richards S., Worley K.C., Hale S., Garria A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Abranch D.M., Marka M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 HLGKGHYSFYSMDIREFOLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                          Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                  TISSUE-Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
Klein S., Gerhard D.S.;
Submitted (JUW-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO74326; AAH7426.1; -.
GO; GO:0008289; F:ltpid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 AA; 52117 MW; 595F36DB5AB8B05D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.8%; Score 394; DB 2;
44.9%; Pred. No. 1.8e-26;
iive 36; Mismatches 60;
    476
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InterPro; IPR00124; LBP_BPI_CETP.
Pfam; PF01273; LBP_BPI_CETP; 1.
Pfam; PF01273; LBP_BPI_CETP; 1.
SWART; SM00328; BPI]; 1.
SWART; SM00329; BPII; 1.
                             Created)
                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                            (TrEMBLrel, 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
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    PRELIMINARY;
                                                                                                                                 Xenopodinae; Xenopus.
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                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                 MGC84153 protein.
                                                                                                                                           NCBI_TaxID=8355;
                                                                              Name=MGC84153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue=Brain,
                            05-JUL-2004
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J. Exp. Med. 164:777-793 (1986).
-!- FUNCTION: Binds to the lipid a moiety of bacterial
-!- FUNCTION: Binds to the lipid a moiety of bacterial
lipopolysaccharides (LSS), a glycolipid present in the outer
membrane of all Gram-negative bacteria. The LBP/LPS complex seems
to interact with the CD14 receptor.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00400; LBP BPI CETP; 1.
Antibiotic; Direct protein sequencing; Glycoprotein; Lipid transport; Signal; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=86306528; PubMed=2427635;
Tobias P.S., Soldau K., Ulevitch R.J.;
"Isolation of a lipopolysaccharide-binding acute phase reactant from
rabbit serum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schumann R.R., Leong S.R., Flaggs G.W., Gray P.W., Wright S.D., Mathison J.C., Tobias P.S., Ulevitch R.J.; "Structure and function of lipopolysaccharide binding protein."; Science 249:1429-1431 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipopolysaccharide-binding protein.
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
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S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E -> G (in Ref. 2).
S -> F (in Ref. 2).
628A6E0A647200C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipopolysaccharide-binding protein precursor (LBP)
                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Search completed: October 21, 2005, 11:30:50 Job time : 66.7154 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

    protein search, using sw model

                      Copyright
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October 21, 2005, 11:22:43 ; Search time 171.285 Seconds (without alignments) 1455.954 Million cell updates/sec OM protein Run on:

US-10-629-516-2 2507 1 MRENMARGPCNAPRWVSLMV.......NVVLQPHQNFLLFGADVVYK 487 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues

Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:*
2: uniprot_trembl:* UniProt 03:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	ption	Q8iw58 homo sapien	P17213 homo sapien	P17453 bos taurus	Q28739 oryctolagus	Q6axu0 rattus norv	Q67e05 mus musculu	-	Q6glx0 xenopus lae	P18428 homo sapien	Q8tcf0 homo sapien		Q61805 mus musculu	_	-				-		Q9gk40 oryctolagus	Q8nfq6 homo sapien	Q8c186 mus musculu		P55065 mus musculu	-	Q8wmn7 sus scrofa	Q66iu4 xenopus lae	Q8wmq5 oryctolagus	_		Q8vyc2 arabidopsis
	ID	O8IW58	BPI HUMAN	BPI_BOVIN	BPI_RABIT	Q6AXU0	Q67E05	QBBSF3	OEGLX0	LBP HUMAN	QSTCF0	LBP RAT	LBP_MOUSE	LBP_RABIT	Q8JFX3	Q8JFX4	080409	Q7T3Q8	Q7T3Q9	Q9GK39	Q9GK40	BPL2 HUMAN	BPL2_MOUSE	PLTP_HUMAN	PLTP_MOUSE	Q817 <u>Z</u> 9	Q8WMN7	Q661U4	Q8WMQ5	Q95JG0	Q6DEI0	Q8VYC2
	DB	5	Н	Н	Н	N	7	C\$	N	-	~	-	ч	ч	~	~	~	~	~	~	~	٦	П	-	-	N	~	N	~	~	7	7
	Query Match Length	487	483	482	445	482	483	486	476	481	477	481	481	482	473	473	473	473	473	179	178	507	509	493	493	477	496	483	503	503	486	515
*	Query	99.7	99.2	64.9	60.1	56.5	54.3	53.8	45.7	43.4	42.4	41.4	41.1	39.3	34.7	34.6	34.6	32.5	32.5	32.3	24.8	21.6	20.0	18.5	18.5	18.0	17.9	17.3	17.3	17.3	17.0	15.4
	Score	2500	2486	1627.5	1507.5	1415.5	1361	1349.5	1145.5	1088	1062	1039	1030	985.5	870.5	867.5	867	814	814	811	621.5	541	500.5	465	463.5	452.5	450	434	433.5	433.5	$\sim$	386.5
	Result No.	7	7	Э	4	ហ	9	7	80	g	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q9maus arabidopsis Q8lal8 arabidopsis	Q9ltr5 arabidopsis P11597 homo sapien Q6uwn3 homo sapien	Q6zme0 homo sapien Q9n019 sus scrofa	P47896 macaca fasc Q8n4f0 homo sapien	P2268/ Oryctolagus Q9bg59 tupaia glis Q05704 rattus norv	
Q9MAU5 Q8lal8	Q9LTRS CETP_HUMAN Q6UWN3	Q6ZME0 Q9N0L9	CETP_MACFA BPIL_HUMAN	CETP RABIT Q9BG59 LPC4 RAT	BPIL_MOUSE BPL3_MOUSE
2 2	2 1 2	0 0		1 77 1	
488 488	1424 493 458	458 127	4.93 458	497 485 470	462
7. 4	12.6 11.8 11.4	m 7	7.7.	8.7.4	4.4.
13	211	77	77	507	22
337.5 336.5	317 295 287	283 282	282	271.5	252.5
32 33	3 8 8 3 5 8	37	39	4 4 4 1 2 6	4 4 5

## ALIGNMENTS

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Poters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malawason R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Maramson R.D., Mullahy S.J.,

RA Rodards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Sanchez A.,

RA Richards J., Helton B., Ketteman M., Maddan A., Souffgues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Minting M., Nadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Temperation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                             Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A..
SINGUEBLOOG;
Strausberg R.;
Submitted (DBC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0409955, AAH40955.1; --
HSSP, P17213; 1EWF.
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InterPro; IPR001124; LBB BPI CETP.
Ffam; PF01273; LBB BPI CETP.
Ffam; PF0286; LBB BPI CETP.C; 1.
SMART; SM00328; BPI1; 1.
SMART; SM00329; BPI2; 1.
PROSITE; PG00400; LBP BPI CETP; 1.
SEQUENCE 487 AA; S3880 WW; FE709D9317E5206D CRC64;
                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Bactericidal/permeability-increasing protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                         487 AA.
                                         PRT;
                                         PRELIMINARY;
                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE=Blood;
                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                        Name=BPI;
                                                               Q8IW58
                                         QBIW58
RESULT 1
                   Q8IW58
ID QE
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Length 487;

DB 2;

99.7%; Score 2500;

Query Match

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'Cloning of cDNA of human bactericidal/permeability-increasing
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                                                           1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
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                      Gaps
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P17213; Q9BYZ9; Q9H1L2; Q9H1M8; Q9H203; Q9UD65;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Bactericidal permeability-increasing protein precursor (BPI) (CAP
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MEDLINE-89255455; PubMed=2722846;
Gray P.W., Flaggs G., Leong S.R., Gumina R.J., Weiss J., Ooi C.E.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 2.26
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Xu J., Wang H.;

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Control of the cycloxic action of BPI is limited to many species of Gram-negative bacteria; this specificity may be explained by a strong affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the negatively charged lipopolysaccharides that are unique to the cram-negative bacterial outer envelope.

C. --- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear leukcoytes (PMN) granules.

C. --- DOMAIN: The N-terminal region may be exposed to the interior of the granule, whereas the C-terminal portion may be embedded in the membrane. During phagocytosis and degranulation, proteases may be released and activated and cleave BPI at the junction of the N-cleaninal portions of the molecule, providing controlled are release of the N-terminal antibacterial fragment when bacteria are
                                                                                                                MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

MEDLING DOPE, Bird C.P., Bates K.N., Beard D.M., Brown A.J.,

MEDLING DOPE, Bird C.P., Butler A.P., Cardr L.N., Clark S.N., Clack C.N., Clamp M., Clark G., Clark L.N., Clark S.N., Clack C.N., Clamp M., Coville G.J., Deadman R.D., Dunn M., Coville G.J., Perakland P.D., Markler D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Almamond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Ray M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Marchan M.A., Lloyd C., Lloyd D.M., Lovell J.D., More M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L., Asmasay H., Stoch C.E., Smith M.L., Socherlund C., Steward C.A., Sulston J.E., Stuce C.D., Smith M.L., Socherlund C., Thomas D.W., Thorpe A., Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A., Asmitchead S.L., Whitteker P., Willey D.L., Williams L., Williams S.A., Willing D.L., Williams L., Willia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comparative analysis of human chromosome 20.";
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Ooi C.E., Weiss J., Elsbach P., Frangione B., Mannion B.;
"A 25-kDa NH2-terminal fragment carries all the antibacterial activities of the human neutrophil 60-kDa bactericidal/permeability-increasing protein.";
J. Biol. Chem. 262:14891-14894(1987).
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MEDLINE-89315847; PubMed=2501794;
Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
Marra M.N., Seeger M., Nathan C.F.;
"Antibiotic proteins of human polymorphonuclear leukocytes.";
Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
process.;;;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   protein.
Cleavage sites for elastase (Potential)
Potential.
V -> A (in dbSNP:1341023).
                                                                                                                                  POTENTIAL

V - A (in dbSNP:1341023).

/FIId=VAR 018401.

A - V (in dbSNP:5743509).

/FIId=VAR 018402.

K - B (in dbSNP:4358188).

/FIId=VAR 018403.

P - S (in Ref. 3).

F - L (in Ref. 3).

K - B (in Ref. 3).

K - R (in Ref. 3).
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385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFYPAVDVQAFAVLDNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNI
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P17453;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 44, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Bactericidal permeability-increasing protein precursor (BPI).
                                                                                                                                                                                                                                                                                                  99.2%; Score 2486; DB 1; Length 483; 100.0%; Pred. No. 2.5e-180; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 483, Conservative
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125 QKRFLKMSGNPDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGW 184
                                LIOLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIK 64
                                                                                                                                                                                                                                                                                                                                                           similarity).

DOMAIN: The N-terminal region may be exposed to the interior of the granula, whereas the C-terminal portion may be embedded in the membrane. During phagocytosis and degranulation, proteases may be released and activated and cleave BPI at the junction of the N-and C-terminal portions of the molecule, providing controlled release of the N-terminal antibacterial fragment when bacteria are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increasing protein (BPI).";
Nucleic Acids Res. 18:3052-3052(1990).
-!- FUNCTION: The cytocoxic action of BPI is limited to many species of Gram-negative bacteria; this specificity may be explained by a serving affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the Gram-negative bacterial outer envelope.
-!- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear Leukocytes (PMM) granules (By similarity).
-!- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By
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N-linked (GLNAc. . .) (Potential).
N-linked (GLNAc. . .) (Potential).
N-linked (GLNAc. . .) (Potential).
N-linked (GLNAc. . .) (Potential).
N-linked (GLNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ingested (By similarity).
SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
               Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bactericidal permeability-increasing
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                                                                                                                             TISSUE=Bone marrow;
MEDLINE=90272418; PubMed=2349103;
Leong S.R., Camerato T.;
"Nucleotide sequence of the bovine bactericidal permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.4e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00400; LEP BPI_CETP; 1.
Antibiotic; Glycoprotein; Membrane; Signal.
SIGNAL
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HSSP; PI7213, 1EWF.
InterPro; IPRO1124; IBP_BPI_CETP.
Pfam; PF02186; IBP_BPI_CETP; 1.
SMART; SM00328; BPII_I.
SMART; SM00329; BPII; 1.
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63.5%;
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62
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375
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482 AA;
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                                                                                                               SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=9913;
                                                                Bovinae; Bos
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SEQUENCE
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65 IPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKA 124 

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                           359
                                                                                                                                                                                                                                        424
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                                                                                                                                                                                                                                                                                                                                                                245 ATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=New Zealand white; TISSUE=Bone marrow;
Weiss J., Weinrauch Y., Levy O., Flynn S.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: The cytocoxic action of BPI is limited to many species
of Gram-negative bacteria; this specificity may be explained by a strong affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the Gram-negative bacterial outer envelope (By similarity).
-!- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear Leukocytes (PMN) granules (By similarity).
-!- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By
                                                                        300 GALNLTLRDDMIPKESKFRLTTKFFGILIPQVAKMFPDMQMQLFIWASLPPKLTMKPSSL
180 LIOLFRKRIESLLOKSMTRKICEVVTSTVSSKLOPYFQTLPVTTKLDKVAGVDYSLVAPP
                                                                                                                                                                                                                                          365 TFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNI
                                                                                                                                                                                                                                                                 GPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ingested (By similarity). SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (Rel. 44, Last annotation update)
Bactericidal permeability-increasing protein (BPI) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 AA
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Hellon B.K., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.;
A "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IPDFSGDFKIKHLGKGTYEFYSMAVEGFHIPDPQIKLLPSDGLQLSITSASIKISGRWKY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 GPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 MTIDKFLEGQLRGEFFWRGHHGPFPAVPPVMNILPNNNYMVCMGISDYFFNTAEFAYQES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 QKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.5%; Score 1415.5; DB 2; Length
55.8%; Pred. No. 5.7e-99;
ive 89; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC079318; AAH99318.1; -. GenBank/DDBJ databases.
EMBL; BC079318; AAH99318.1; -. GO; GO:0008289; F:11ptd binding; IEA.
InterPro; IFR001124; LBP BPI CETP.
Pfam; PF01273; LBP BPI CETP; 1. SMART; SM00329; BPII; 1. SMART; SM00329; BPII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53751 MW; 269591C4C2F5A6D1 CRC64;
                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Q67E05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461
                                                                                                                                                                                                                                                                                                                                                                                                                                           42 QKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISM 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 VPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTLPVMTKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHHNPPPFRAPPVMEFPAAH 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 KADKLVGELTLGRLILELKHSNIGSFPVQLLQALMDYVLSAVVLPKVNEKLQRGLPLFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRMVYLGLSDYFFNTAGLVYQBAGVLKMTLRDDMIPKBSKFRLTTKFFGTFLPEVAKKFP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Potential.
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PubMed=1247932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                352 N-linked (GlcNAc. . .) (Potential)
48837 MW; 209AE0894FEDACFC CRC64;
                                                                                                                                                                                                                                                                                                                                                             445;
                                                                                                                                                                                                                                                                                                                                                           DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                     83; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Bactericidal/permeability-increasing protein.
                                                                                                                                                                                                                                                                                                                                                         60.1%; Score 1507.5; DB 1
63.0%; Pred. No. 5.2e-106;
ive 80; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                        Interpro; IPRO01124; LBP BPI CETP.
Pfam; PF01273; LBP BPI CETP; 1.
Pfam; PR02886; LBP BPI CETP C; 1.
SMART; SM00328; BPI1; 1.
SMART; SM00329; BPI2; 1.
PROSITE; PS00400; LBP BPI CETP; PARTIAL.
Antibiotic; Glycoprotein; Transmembrane.
              습.
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            send an email to license@isb-sib.
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                                                  EMBL; U61270; AAB03812.1; -.
HSSP; P17213; 1BP1.
                                                                                                                                                                                                                                                                                                                                                             Query Match 60.1
Best Local Similarity 63.0
Matches 279; Conservative
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                                                                                                                                                                                                                                                                                                  352 3
445 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKL-DRLLLELKHSN 423
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                                                                                                                                                                                                                                                                                      65 IPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKA 124
                                                                                                                                                                                                                                                                                                                            OKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGW 184
                                                                                                                                                                                                                                                                                                                                                                   LIQLFHKKIESALRNKWNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPP 244
                                                                                                                                                                                                                                                                                                                                                                                                        245 ATTAETLDVOMKGEFYSENHHNPPPFRAPPVMEFPAAHDRWYLGLSDYFFNTAGLVYQEA 304
                                                                                                                                                                                                                                               5 MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIK 64
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                                                                                                                                                                                                                            Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male epididymis cDNA, RIKEN full-length enriched
11brary, clone:9230105K17 product:weakly similar to
bactericidal/permeability-increasing protein.
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                            2;
                                                                                                                                                                                                        DB 2; Length 483;
                                                                                                                                                                                                       54.3%; Score 1361; DB 2; Length 4
54.1%; Pred. No. 8e-95;
ive 90; Mismatches 129; Indels
                                                                                              STRAIN-Swiss Webster;
Bingle C.D., Craven J.;
Bingle C.D., Craven J.;
Bungle C.D., Craven J.;
Bubmitced (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY363931, AAR13289.1; -.
InterPro; IPR001124; LBP BPI_CETP.
Pfam; PP01273; LBP BPI_CETP. J.
Pfam; PP02886; LBP BPI_CETP_C; 1.
SWART; SM00329; BPI2; 1.
                                                                                                                                                                                     483 AA; 53940 MW; 4AA2D48095C52B74 CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Bactericidal/permeability-increasing protein.
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                                                                                                                                                                                                                   al Similarity 54.13
260; Conservative
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                                       Mus musculus (Mouse)
                                                                                      SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                      SEQUENCE
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Q8BSF3;
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DEPORTY
STRAIN=CS-FLAC); TISSUE=Epididymis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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w genes.";
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                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUB=Epididymis;
MEDINE=9927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/61; TISSUB=Epididymis; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata Y., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunia N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matamunoto H., Sakaguchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Rikki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUE=Epididymis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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GO; GO:0008289; F:lipid binding; IEA
InterPro; IPR001124; LBP BPI CETP.
Ffam; PF021273; LBP BPI CETP.
Ffam; PF02886; LBP BPI CETP.
SWART; SW00328; BPII; I.
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                                                                                                                                                                                                                                                                                                                                                        Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
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                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTWAPDNVRKWSALLLLAIIGTALTAATDPGFVAMISQKGLDPACQQGVVELQAIS
                                                                                                                                                                                                                         5 MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIK
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                                                                                  Gaps
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Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                          Length
                                        53.8%; Score 1349.5; DB 2; Length
53.7%; Pred. No. 6e-94;
.ive 90; Mismatches 129; Indels
54351 MW; 9D8F627EA5496D62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MGC84153 protein.
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                                                                                  Conservative
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    486 AA;
                                                             Similarity
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTFYPAVDVQAFAVLPNSSLASLFLIGMITTGSMEVSAESNRLVGELKLDRLLLELKHSN
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                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                    "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xiein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO74326; AA474326-1;
GO; GO:0008289; F:11pid binding; IEA.
InterPro; IPR00129; F11i.
InterPro; IPR00129; F11i.
InterPro; IPR001124; LBP_BPI_CETP.
Pfam; PF01373; LBP_BPI_CETP; 1.
Pfam; PF01273; LBP_BPI_CETP? 1.
Rean; PF02886; LBP_BPI_CETP_C; 1.
SWART; SW00329; BPI1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 AA; 52117 MW; 595F36DB5AB8B05D CRC64;
                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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A MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
A MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
A Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
A Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
A Bailey J., Barlow K.F., Bates K.N., Basre D.M.,
Bassley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder N.P.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
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Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
A Hunmond S., Harley J.L., Heach P.D., Ho S., Holden J.L., Howden P.J.,
A Hurthe E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knighte A., Laird G.K., Lawlor S.,
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                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                  LBP_HUMAN STANDARD; PRT; 481 AA. P18428; Q9438; Q92672; Q9H403; Q9UD66; CA. Created) CRel. 16, Created) Cres. 15-DEC-1998 (Rel. 37, Last sequence update) O5-JUL-2004 (Rel. 44, Last annotation update) Lipopolygaccharide-binding protein precursor (LBP)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch). Process Sci. 7:906-914(1998).
-!- FUNCTION: Bainds to the lipid a moiety of bacterial
-!- FUNCTION: Bainds to the lipid a glycolipid present in the outer
membrane of all Gram-negative bacteria. The LBP/LPS complex seems
to interact with the CD14 receptor.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A. Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S. Rogers J.; "The DNA sequence and comparative analysis of human chromosome 20."; MEDINE-99227852; PubMed-9568897; Beamer L.J., Carroll S.F., Eisenberg D.; "The BPI/LBP family of proteins: a structural analysis of conserved Sufton C.L., Smith R.I.F., Centola M.B., Theofan G.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0006953; P:acute-phase response; TAS.
GO; GO:0006968; P:cellular defense response; TAS.
GO; GO:00069618; P:response to pathogenic bacteria; TAS.
InterPro; IPR001124; LBP_BPI_CETP. L, AF013502, AAC39547.1; JOINED. L, AF013502, AAC39547.1; JOINED. L, AF013504, AAC39547.1; JOINED. L, AF013505, AAC39547.1; JOINED. L, AF013505, AAC39547.1; JOINED. L, AF013507, AAC39547.1; JOINED. L, AF013509; AAC39547.1; JOINED. L, AF013509; AAC39547.1; JOINED. L, AF013511; AAC39547.1; JOINED. L, AF013511; AAC39547.1; JOINED. L, AF105067; AAD31962.1; EMBL; M35533; AAA59493.1; EMBL; X98657; CAA67226.1; EMBL; X98659; CAA67226.1; EMBL; X98659; CAA67226.1; JOINED.
EMBL; X98660; CAA67226.1; JOINED.
EMBL; X98661; CAA67226.1; JOINED.
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EMBL; X98665; CAA67226.1; JOINED. JOINED. CAC10462.1; -. L42172; AAA66446.1; -. AF013512; AAC39547.1; AAC39547.1; SEQUENCE OF 1-41 FROM N.A. Nature 414:865-871(2001). Genew; HGNC:6517; LBP. MIM; 151990; -. 3D-STRUCTURE MODELING. PIR; A35843; A35843. PIR; A54136; A54136. HSSP; P17213; 1EWF. AL080249; family. regions." EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; 

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                         (Potential).
(Potential).
(Potential).
Pfam; PF01273; LBP_BPI_CETP; 1.
Pfam; PF02886; LBP_BPI_CETP_C; 1.
SMART; SM00228; BPII; 1.
SMART; SM00329; BPIZ; 1.
PROSITE; PS00400; LBP_BPI_CETP; 1.
Antibiotic; Glycoprotein; Lipid transport; Signal; Transmembrane.
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VTAS -> GYCL (in Ref. 1) .
L -> S (in Ref. 1) .
L -> S (in Ref. 1) .
R -> S (in Ref. 1) .
L -> S (in Ref. 1) .
L -> H (in Ref. 4) .
VWSLP -> H (in Ref. 1) .
L -> H (in Ref. 4) .
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Attaubberg R.L., Feingold B.A., Grouse L.H., Dorge J.G., Straubberg R.L., Feingold B.A., Grouse L.H., Dorge J.G., Straubberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D., Antschul R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F., Bhat N.K., Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Brokerts M.S., McZwan P.J., McKernan K.J., Malke J.A., Gunaarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahay J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Schmutz J., Myers R.M., Butterfield Y.S., A Nores S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein J.E., Schein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 GRGRYEFHSLNIHSCELLHSALRPVPGQGLSLSISDSSIRVQGRWKVRKSFFKLQGSFDV 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAETLDVQMKG 257
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TISSUE-Liver;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC022256; AAH22256.1;
HSSP; P17213; 1EWF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0008289; F:lipid binding; IEA.
InterPro; IPR001124; LBP BPI CETP.
Pfam; PF01204; LBP BPI CETP.
Ffam; PF02086; LBP BPI CETP.C; 1.
SMART; SM00328; BPI; 1.
PR081T; SM00329; BPI; 1.
PR081TE; PS004000; LBP BPI CETP; 1.
SEQUENCE 477 AA; SE3933 WW; 03DSE9D55A3BA6D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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A MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

BA Grapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley W.C., Shevchenko Y., Bouffard G.G.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schaefer A.C., Grimwood J., Schmutz J., Myers R.M.,

R Scherztical Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                     365 EGFVILPSSARESVFRLGVVTNVFVSLTFDNSKVTGMLHPEKAQVRLIESKVGMFNVNLF 424
GSFDLDVKSVTISVDLLLGVDP-SERPTVTASGCSNRIRDLELHVS-GNVGWLANLFHNQ 184
                                                                                                      VOMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLR 312
                                                                                                                                                                                                           245 VMFKGEIFNRNHRSPVTTPTPTMSLPEDSKQMVYFAISDQAFNIATRVYHQAGYLNFTIT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Binds to the lipid a molety of bacterial lipopolysaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. The LBP/LPS complex seems to interact with the CD14 receptor.
                                                                          IESALRNKANSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAETLD
                                                                                                                                                                                                                                                                           DDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDV
                                                                                                                                                                                                                                                                                                                                                                        373 QAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/C;
MEDLINE=97289150; PubMed=9144073;
MEDLINE=97289150; DibMed=91144073;
Ulengacher S., Jongeneel C.V., le Roy D., Lee J.D., Kravchenko V.,
Ulevitch R.J., Glauser M.P., Heumann D.;
"Reactivity of murine and human recombinant LPS-binding protein (LBP)
within LPS and Gram-negative bacteria.";
J. Inflamm. 47:165-172(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus muserius (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LBP MOUSE

1D LBP MOUSE

AC 061805; 099KA0;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

E Lipopolysaccharide-binding protein precursor (LBP).
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                                                                               193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUB-Liver; MEDLINE-94292804; PubMed-8021509; SL G.L., Freeswick P.D., Geller. D.A., Wang Q., Shapiro R.A., Wan Y.H., Billar T.R., Tweardy D.J., Simmons R.L., Wang S.C.; Molecular cloning, characterization, and tissue distribution of rat lipopolysaccharide binding protein. Evidence for extrahepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 153:743-752(1994).

-!- FUNCTION: Binds to the lipid a moiety of bacterial lipopolypaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. The LBP/LPS complex seems to interact with the CD14 receptor.

-!- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
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PIR; 156246, 156246.
HSSP: P17213b; LEWF.
RGD; 61865; Lbp.
InterPro; 1PR001124; LBP_BPI_CETP.
Pfam; PF001273; LBP_BPI_CETP_C; 1.
Pfam; PF001273; LBP_BPI_CETP_C; 1.
SMART; SM00328; BPI1; 1.
SMART; SM00328; BPI2; 1.
PROSITE; PS00400; LBP_BPI_CETP; 1.
PROSITE; PS00400; LBP_BPI_CETP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 Lipopolygaccharide-binding protein
300 N-linked (GlcNAc. . .) (Potential).
355 N-linked (GlcNAc. . . .)
53600 WW, 23867CB9CC97DZFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 481;
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109; Mismatches 166; Indels
     063313;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Lipopolysaccharide-binding protein precursor (LBP)
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                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
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355 3
481 AA;
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197; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression.";
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Best Local S:
Matches 197
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipopolysaccharide-binding protein.
N-linked (GlcNAc. .) (Potential).
N-linked (GLNAc. .) (Potential).
C -> G (in Ref. 2).
K -> G (in Ref. 2).
R -> S (in Ref. 2).
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34EA9C066C9AB678 CRC64;
                                                                                                                                                                                                                                       EMBL; X99347; CAA67727.1; -.
EMBL; BC004795; AAH04795.1; -.
HSSP; P17213; IEWF.
MGD; MGI:1008776; Lbp.
GO; GO:0001530; F:lipopolysaccharide binding; IDA.
InterPro; IRR001124; LbP BPI CETP.
Pfam; PF01273; LBP EMI CETP.
Ffam; PR0286; LBP EMI CETP.
SMART; SM00329; BFI1; I.
PROSTE; PS00400; LBP BPI CETP;
Antibiotic; Glycoprotein; Lipid transport; Signal; Transport; Signal; Transport; Signal; Transportic; Glycoprotein; Lipid transport; Signal; Transportic; Companients
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Antibiotic; Direct protein sequencing; Glycoprotein; Lipid transport;
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                             478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. EXP. Med. 164:777-793 (1986).

-!- FUNCTION: Binds to the lipid a moiety of bacterial lipopolysaccharides (LPB), a glycolipid present in the outer membrane of all Gram-negative bacteria. The LBP/LPS complex st to interact with the CD14 receptor.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schumann R.R., Leong S.R., Flaggs G.W., Gray P.W., Wright S.D., Mathison J.C., Tobias P.S., Ulevitch R.J.; "Structure and function of lipopolysaccharide binding protein."; Science 249:1429-1431 (1990).
Lipopolysaccharide-binding protein N-linked (GIGNAc. .) (Potential) N-linked (GIGNAc. . .) (Potential) N-linked (GIGNAc. . .) (Potential)
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
NCBI_TaxID=9986;
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                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Lipopolysaccharide-binding protein precursor (LBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 40.9%; Pred. No. 2.7e-66;
Matches 193; Conservative 103; Mismatches 171;
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Pred. No. 2.7
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PIR; B35843; B35843.
HSSP; P17213; 1EWF.
InterPro; IPR001124; LBP_BPI_CETP.
Pfam; PP01273; LBP_BPI_CETP; ISMART; SM00328; BPII; ISMART; SM00329; BPII; I.
                                                                                                                                                             PRT;
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MEDLINE=90385281; PubMed=2402637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86306528; PubMed=2427635;
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54001 MW;
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TISSUE=Serum;
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                                                                                                                                                                                      353 ASGTVTAYAIQPNTTLSPLFVLNMEGSVSAQMNVTGVKLAGAITLNKIEMTLGTSYVGQF 412
                                                                                                                                                                                                                                                                              LFHKKIESALRNKANSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATT 247
                                                                                                                                                                                                                                                                                                                                                                                                         248 AETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 KMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFY 367
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                             SDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQK-R 127
                                                                                                                                                     FLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQ 187
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A Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y.,

A Inagawa H., Honda T., Kohchi C., Soma G.,

A A Inagawa H., Honda T., Kohchi C.,

Inagalian T., Yokomizo Y., Soma G.,

"Cloning and characterization of the homolog of mammalian

Inpopolysaccharide-binding protein and bactericidal permeability-

Increasing protein in rainbow trout Oncorhynchus mykiss.";

J. Immunol. 168:5638-5644(2002).

EMBL; AB042025; BAB91243.1; -.

R HSSP; P17213; LBWF

R GO; GO:0008289; F:lipid binding; IEA.

InterPro; IPR001124; LBP_BPI_CETP.

R Pfam; PF0286; LBP_BPI_CETP.

R Pfam; PF0286; LBP_BPI_CETP.

R Pfam; PF0286; LBP_BPII; I.

SMART; SM00328; BPII; I.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
LBP (LPS binding protein)/BPI (Bactericidal/permeability-increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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llarity 35.1%; Pred. No. 2.5e-57;
Conservative 119; Mismatches 181;
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Best Local Similarity
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                                                                                           HLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNF 135
                                                                                                                                                                                                                          DLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKIES 195
                                                                                                                                                                                                                                                                                                                                                  ALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATTAETLDVQM 255
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A Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y.,
Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y.,
Inagama H., Yokomizo Y., Soma G.;
I "Cloning and characterization of the homolog of mammalian
I propolysaccharide-binding protein and bactericidal permeability-
I increasing protein in rainbow trout Oncorhynchus mykiss.";
J. Immunol. 168:5638-5644(2002).
R RSEP; BAB91244.1; -.
R RSEP; 17213; IEWF.
R GO, GO:0008289; F:lipid binding; IEA.
R Incerpo; IPR001124; LBP BPI_CETP.
R Pfam; PF0286; LBP BPI_CETP.
R Pfam; PF0286; LBP BPI_CETP_C; I.
SWART; SM00328; BPII; I.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
LBP (LPS binding protein)/BPI (Bactericidal/permeability-increasing
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei;
Protacanthopterygii, Salmoniformes; Salmonidae; Oncorhynchus.
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llarity 35.3%; Pred. No. 1.5e-57;
Conservative 121; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 AA
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Name=LBP/BPI-2;
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188 LFHKKIESALENKANSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGLVAPPATT 247

174 LFSAYIDKALRSALQKQICPLVADTITD-MNPHLKTLNVLAKVDKYAEVEYSMVTSPTIS 232
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                                                                                                                                                       FLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQ 187
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Search completed: October 21, 2005, 11:30:48 Job time : 174.285 secs

4.

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

- protein search, using sw model OM protein October 21, 2005, 11:22:43 ; Search time 14.2593 Seconds (without alignments) 1241.566 Million cell updates/sec Run on:

US-10-629-516-2_COPY_10_193

943 1 CNAPRWVSLMVLVAIGTAVT......HVHISKSKVGWLIQLFHKKI 184 Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	08	ID	Description
7	943	100.0	487	2	A30909	bactericidal/perme
8	832	88.2	250	4	843383	bactericidal/perme
m	596.5	63.3	482	N	S10180	bactericidal perme
4		45.6	481	~	A54136 -	ᆽ
ഗ	428	45.4	481	N	I56246 ·	lipopolysaccharide
9	416	44.1	477	N	A35843	lipopolysaccharide
7	357.5	37.9	482		B35843	lipopolysaccharide
80	ς.	18.3	493		149370	plasma phospholipi
6	169	17.9	493		A53533	phospholipid trans
10	130.5	13.8	493		A26941	cholesteryl ester
11	129.5	13.7	497		146692	cholesteryl ester
12	120.5	12.8	493		A53176	cholesteryl ester
13	110	11.7	576	7	T22700	hypothetical prote
14	102	10.8	909	N	T29190	ical
15	98.5	10.4	824		E87856	_
16	98.5	10.4	846	~	T20710	hypothetical prote
17	95	10.1	488		C86183	
18	92	9.8	464		T16889	
19	90.5	9.6	486		T20482	hypothetical prote
20	89	9.4	827		D96907	ated
21	84.5	9.0	1169		G72571	DNA-
22	84	8.9	405		D84871	probable polygalac
23	82.5	8.7	498		B99946	
24	82.5	8.7	573		S50627	_
25	82.5	8.7	2218		B84683	_
26	82	8.7	554		T15438	hypothetical prote
27	82	8.7	1120	~	T38431	irected
28	81.5	9.6	1902		C97702	
29	80	8.5	440	~	B71162	hypothetical prote

MG096 homolog D09_ hypothetical prote hypothetical prote	ornithine decarbox hypothetical prote conserved hypothet	hypothetical prote probable formamido	hypothetical prote probable formamido inorganic diphosph	soluble hydrogenas probable ligand-bi probable cytochrom	probable cucumisin conserved hypothet
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# ALIGNMENTS

bactericidal/permeability-increasing protein precursor - human N;Alternate names: 55K bactericidal protein

C;Species: Homo sapiens (man)
C;Date: 18-Apr-1989 #text-change 09-Jul-2004
C;Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text-change 09-Jul-2004
C;Accession: A33850; B54136; A29464; A43600; A49716; A30509)
C;Accession: A33850; B54136; A29464; A43600; A49716; A30509)
P; Figray, P.W.; Flagge, G.; Leong, S.R.; Gumina, R.J.; Weifsg; J.; Ooi, C.E.; Elsbach, P.
J; Biol. Chem. 264, 9505-9509, 1989
A; Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and A;Reference number: A33850; MUID:89255455; PMID:2722846

A; Accession: A33850

A; Molecule type: mRNA A; Residues: 1-487 -GRAA. A; Residues: 1-487 -GRAA. A; Cross-references: UNIPROT: Q9UCT4; GB: J04739; NID: G179528; PIDN: AAAS1841.1; PID: G179529 R; Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon R; Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon A; Mille: Bactericidal/permeability-incressing protein and lipopolysaccharide (LPS)-bindi A; Reference number: A54136; MUID: 94292492; PMID: 7517198

A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA A; Accession: B54136

A;Residues: 1-374,'L',376-487 <WIL>
A;Experimental source: HL-60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:149855)

R;Ooi, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B. © J. Biol. Chem. 262, 14891-14894, 1987 A;Title: A 25-kDa amino-terminal fragment carries all the antibacterial activities of th A;Reference number: A29464; MUID:88033057; PMID:3667613

A; Accession: A29464

A; Molecule type: protein
A; Residues: 32-51 <001>
A; Residues: 32-51 <001>
A; Experimental source: neutrophils
B; Wasiluk, K.R.; Skubitz, K.M.; Gray, B.H.
Infect. Immun. 59, 4193-4200, 1991
A; Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar A; Reference number: A43600; MUID:92040097; PMID:1937776

A; Accession: A43600

A;Molecule type: protein
A;Residues: 32-52, R' <WAS>
A;Residues: 32-52, R' <WAS>
A;Little, R.G.; Kelner, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J.

A;Little, T.G.; Kelner, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J.

A; J. Biol. Chem. 269, 1865-1872, 1994
A;Title: Functional domains of recombinant bactericidal/permeability increasing protein A;Reference number: A49716; MUID:94124531; PMID:8294435

A;Molecule type: protein A;Residues: 32-130;132-141;143-165;202-215,'E',217-225 <LIT> C;Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-as C;Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-as which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysaccha between BPI and an LPS-binding protein from liver and cholesteryl ester transfer protein

A;Gene: GDB:BPI C, Genetics:

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Query Match
Best Local Similarity
Matches 82; Conserv
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C;Date: 3.1-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10180
R;Leong, S.R.; Camerato, T.
Nucleic Acids Res. 18, 3052, 1990
A;Title: Nucleotide sequence of the bovine bactericidal permeability increasing protein A;Reference number: S10180; MUD:90272418; PMID:2349103
A,Cross-references: GDB:131572; OMIM:109195
A;Map position: 20q11.23-20q12
C;Superfamily: lipopolysacchaide-binding protein
C;Superfamily: lipopolysacchaide-binding protein
C;Keywords: antibacterial; cytotoxin; glycoprotein; heparin binding; neutrophil
F;1-31/Domain: signal sequence #status predicted <SIG>F;1-31/Domain: signal sequence #status predicted <SIG>F;32-51/Region: bactericidal permeability-increasing protein #status predicted <MAT>F;32-51/Region: bactericidal #status predicted
F;380/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bactericidal/permeability-increasing protein - synthetic

bactericidal/permeability-increasing protein - synthetic

c; Species: synthetic

d; Note: Home sapiens (man) gene engineered and expressed in Escherichia coli

c; Date: 20-Oct-1994 #sequence_revision 15-Feb-1996 #text_change 15-Feb-1996

C; Date: 20-Oct-1994 #sequence_revision 15-Feb-1996 #text_change 15-Feb-1996

C; Date: 20-Oct-1994 #sequence_revision 15-Feb-1996 #text_change 15-Feb-1996

B; Oct, S, Y; Li, Y; O'Connor, C.D.

B; Dichem. J. 298, 711-718, 1994

A; Title: The region around residue 115 of human bactericidal/permeability-increasing is agene coding for the active domain and characterization of recombinant proteins.

A; Accession: S43383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180
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bactericidal permeability-increasing protein precursor - bovine
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Pred. No. 5.4e-68;
0; Mismatches 0;
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100.0%; Pred
0; M
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Matches 184; Conservative (
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lipopolysaccharide binding protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26.Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156246
R;Su, G.L.; Freeswick, P.D.; Geller, D.A.; Wang, Q.; Shapiro, R.A.; Wan, Y.H.; Billiar, J
                                                                                                                           protein #status predicted <MAT>
                                                            NID:g138; PIDN:CAA36797.1; PID:g139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 FKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKM 122
                                                                                                                                                                                                                                                                                                                                                                                        126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
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                                                                                                                                                                       Length 482;
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1 Similarity 46.6%; Pred. No. 3.5e-31;
82; Conservative 38; Mismatches 54; Indels
                                                                                                                                                                                                                Indels
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A; Note: sequence extracted from NCBI backbone (NCBIP:149401)
A, Accession: S10180
A, Molecule type: mRNA
A, Residues: 1-482 <LEGO>
A, Cross-references: UNIPROT:P17453; EMBL:X52563; NID:g1
C, Superfamily: lipopolysaccharide-binding procesin
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-482/product: bactericidal permeability increasing
                                                                                                                                                                       DB 2;
                                                                                                                                                                     Query Match
63.3%; Score 596.5; DB 2
Best Local Similarity 63.2%; Pred. No. 2.8e-46;
Matches 115; Conservative 29; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Note: sequence extracted from NCBI backbone (NCI
C,Superfamily: lipopolysaccharide-binding protein
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Local Similarity
nes 73; Conserv
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A35843
11popolysaccharide-binding protein - human
C;Species: Homo sapiens (man)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35843
R;Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T
Science 249, 1429-1431, 1990
A;Title: Structure and function of lipopolysaccharide binding protein.
A;Recession: A35843
A;Reference number: A35843; MUID:90385281; PMID:2402637
A;Accession: A35843
A;Status: preliminary
A;Residues: 1-477
C;Genetics:
A;Cross-references: UNIPROT:P18428; GB:M35533; NID:g186965; PIDN:AAA59493.1; PID:g186966
C;Genetics:
A;Gene: GDB:LBP
A;Cross-references: GDB:L33-20q12
C;Superfamily: lipopolysaccharide-binding protein
J. Immunol. 153, 743-752, 1994
A;Title: Molecular cloning, characterization, and tissue distribution of rat lipopolysac A;Title: Molecular cloning, characterization, and tissue distribution of rat lipopolysac A;Reference number: 156246; MUID: 94292804; PMID: 8021509
A;Accession: 156246
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-481 <RES>
A;Cross-references: UNIPROT: 063313; GB:L32132; NID: 9510714; PIDN: AAA21835.1; PID: 9510715
C;Superfamily: lipopolysaccharide-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 GSPDLDVKSVTISVDLLLGVDP-SERPTVTASGCSNRIRDLELHVS-GNVGWLANLFHNQ 184
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                                                                                                                                                                                                        Length 481;
                                                                                                                                                                                                      45.4%; Score 428; DB 2; Length 48
44.2%; Pred. No. 5.4e-31;
tive 45; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Indels
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44.1%; Score 416; DB 2;
Best Local Similarity 46.0%; Pred. No. 6.5e-30;
Matches 81; Conservative 36; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lipopolysaccharide-binding protein - rabbit
C, Species: Oryctolagus cuniculus (domestic rabbit)
                                                                                                                                                                                                      Query Match
Best Local Similarity 44.21
Matches 80; Conservative
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C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004
C;Accession: B35843; A4653
R;Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T
Science 249, 1429-1431, 1990
A;Fitle: Structure and function of lipopolysaccharide binding protein.
A;Reference number: A35843; MUD:90385281; PMID:2402637
A;Accession: B35843
A;Accession: B35843
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A;Residues 1-493 ARBS-
A;Cross-references: UNIPROT:P55065; EMBL:U37226; NID:g1051265; PIDN:AAA80542.1; PID:g105
C;Superfamily: lipopolysaccharide-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLYVKGLTISVHLVLGSE-SSGRPTVTTSSCSSDIQNVELDI-EGDLEELLNLLQSQ1 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LMVLVAIGTAVTAAVN---PGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.3%; Score 172.5; DB 2; 28.8%; Pred. No. 8.4e-08; tive 40; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 357.5; DB 2
Pred. No. 1.3e-24;
9; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 27-53, XG', S8-62,' P',64-65 <TOB>
C;Superfamily: lipopolysaccharide-binding protein
C;Kowords: acute phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.9%;
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Best Local Similarity 28.84
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146692
R;Nagashima, M.; McLean, J.W.; Lawn, R.M.
J. Lipid Res. 29, 1643-1649, 1988
A;Nagashima, M.; McLean, J.W.; Lawn, R.M.
A;Ntle: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protes)
A;Accession: 146692
A;Accession: 146692
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Mclecule type: mRNA
A;Residues: 1-497 <NAGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cholesteryl ester transfer protein - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 07-May-1999
C;Accession: A53176
R;Pape, M.E.; Rehberg, E.F.; Marotti, K.R.; Melchior, G.W.
Arterioscler. Thromb. 11, 1759-1771, 1991
A;Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl est asma high density lipoprotein levels.
A;Reference number: A53176; MUID:92031355; PMID:1931878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P22687; GB:M27486; NID:g530906; PIDN:AAA31199.1; PID:g530907
C;Genetics:
A;Gene: CETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SHLSIASSQVELVDAKTIDVAIQNVSVVFKGTLNYSYTSAWG-----LGINQSVDFEIDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSSQISMVPNVGLKFSISNANIKISGKWK---AQKRFLKMSGNFDLSIEGMSISADLKLG 142
                                          125 GIDQSIDFEIDS---AIDLQINTQLTCDSGRVRTDAPDCYLSFHKLLLHLQGEREPGWIK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 REFQLPSSQISMVPNVGLKFSISNANIKISG-----KWKAQKRFLKMSGNFDLSIEG 132
          121 KMSGNFDLSIEGMSISADLKLGSNPT--SGKPTITCSSCSSHINSVHVHI-SKSKVGWLI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ASYEAGIVCRITKPALLVINQETAKVVQTAFQRAGYPDVSGERAVMLLGRVKYGLHNLQI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 GIVCRÍTKPALLVINQETAKVIQSAFQRANYPNITGEKAMMLLGQVKÝGLHNIQÍSHLSI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 MSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKV------GWLIQLF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GVVVRISOKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 497;
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13.7%; Score 129.5; DB 2;
Best Local Similarity 22.5%; Pred. No. 0.00068;
Matches 40; Conservative 35; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.8%; Score 120.5; DB 2; Best Local Similarity 22.4%; Pred. No. 0.0044; Matches 36; Conservative 36; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M86343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-493 <PAP>
                                                                                                                     178 QLF 180
                                                                                                                                                                     182 OLF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A53176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
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A;Residues: 1-493 <DAY>
A;Cross-references: UNIPROT:P55058; GB:L26232; NID:g468325; PIDN:AAA36443.1; PID:g468326
phospholipid transfer protein precursor - human
N.Alternate names: lipid transfer protein II; PLTP
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A53533
R;Day, J.R.; Albers, J.J.; Lofton-Day, C.E.; Gilbert, T.L.; Ching, A.F.T.; Grant, F.J.;
J. Biol. Chem. 269, 9388-9391, 1994
A;Title: Complete cDNA encoding human phospholipid transfer protein from human endotheli
A;Reference number: A53533; MUID:94179366; PMID:8132678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 FQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 KIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWK---AQKRFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 SLMVLVAIGTAVTAAV----NPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.)Cross-references: GDB:119773; OMIM:118470
A;Map position: 16q13-16q13
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-493/Product: cholesteryl ester transfer protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 PGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGH--YSFYSMDIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 20pter-20qter
C.Superfamily: lipopolysaccharide-binding protein
C.Keywords: glycoprotein
C.Keywords: glycoprotein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-493/Product: phospholipid transfer protein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.9%; Score 169; DB 2; Length 493; 28.7%; Pred. No. 1.8e-07; ive 32; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:340911; OMIM:172425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNPTSGKPTITCSSCSSHINSVH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | : : : | | : : : | RDP-AGRMKVSNVSCQASVSRMH 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 28.7%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: CETP
                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: GDB:PLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Genetics:
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protein F10D11.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B87856
C;Accession: B87856
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A7500; MUID:99069613; PMID:9851916
A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elcA;Note: published errata appeared in Science 283, 15, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: 017781; GB: chr_I; PIDN: CAB02917.1; PID: 93875779; GSPDB: GN000 C; Genetics:
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                                                                                                                                                   FSISNANIKISGKWKAQKRF---LKMSGNFDLSIEGMS--ISADLKLGSNPTSGKPTITC 154
                                                                                                                                                                                                 ::: | : | : | : | : | : | : | : | 118 WTMQNMDIGLLGDLSGSVNIVVPLNLTGQVEILAQGLTFHLESSIEKGKN---GSAKVTS 174
44 TAALQKELKRIKIPDYS----DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 PGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQ
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21.6%; Pred. No. 0.81;
live 29; Mismatches 78;
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hypochetical protein F55B12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Tacor-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22700
R;Sims, M.
submitted to the EMBL Data Library, September 1996
A;Reference number: 219602
A;Reference number: 219602
A;Reference proper DNA
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-576 <WIL>
A;Coss-references: UNIPROT:093796; EMBL:279757; PIDN:CAB02126.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F55B12
C;Genetics:
A;Gene: CESP:F55B12.5
A;Map position: 5
A;Introns: 47/1; 178/3; 290/3; 353/2; 384/2; 427/3
A;Introns: 47/1; 178/3; Caenorhabditis elegans hypothetical protein F55B12.5
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Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 172919
Riwoessne, J.; Stellyes, L.
Riwoessne, J.; Stellyes, L.
A; Reference number: 220585
A; Reference number: 220585
A; Recession: T29190
A; Recession: T29190
A; Recession: T29190
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-606 <WOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%; Score 110; DB 2; Length 576; 22.9%; Pred. No. 0.048; tive 30; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHIS 169
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                                                                                              SNPT--SGKPTITCSSCSSHINSVHVHI-SKSKVGWLIQLF
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October 21, 2005, 11:22:38; Search time 170.559 Seconds (without alignments) 1104.324 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-629-516-2 2507 1 MRENWARGPCNAPRWVSLMV......NVVLQPHQNFLLFGADVVYK 487 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2003as:*

7: geneseqp2003as:*

8: geneseqp2003as:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2507 2507 2507 2507 2507 2507	100.0 487	7	AAW05852	Aaw05852 Recombina
2507 2507 2507 2507 2507 2507	100.0 487	0	AAR97568	Aar97568 Human bac
2507 2507 2507 2507 2507	100.0 487	7	AAW17987	Aaw17987 Bacterici
2507 2507 2507 2507 2507	100.0 487	0	AAW44650	Aaw44650 Human bac
2507 2507 2507 2507	100.0 487	0	AAW01702	Aaw01702 Human bac
2507 2507 2507	100.0 487	~	AAW17986	Aaw17986 Human bac
	100.0 487	~	AAW47090	Aaw47090 Human bac
	100.0 487	7	AAW40141	Aaw40141 Human rec
	100.0 487	7	AAW61158	Aaw61158 Recombina
	100.0 487	~	AAW56156	Aaw56156 A bacteri
24 2507 10	100.0 487	7	AAW26776	Aaw26776 Human bac
25 2507 10	100.0 487	~	AAW63306	Aaw63306 Recombina

487 2 AAW63304 487 2 AAW41359 487 2 AAW31621 487 2 AAY31621 487 2 AAY31621 487 2 AAY31621 487 3 AAY8385 487 3 AAY83169 487 3 AAB16189 487 3 AAB16189 487 3 AAB18762 487 3 AAB1335 487 4 AAR09357 487 4 AAR09357 487 4 AAR0916	Aaw61304 Human bac Aaw41159 Human bac Aaw11864 Human bac Aay17864 Human bac Aay21631 Human bac Aay21630 Recombina Aaw98885 Human BPI Aay81169 Human BPI Aay81169 Human bac Aab16109 Human bac Aab16109 Human bac Aab16109 Human bac Aab16109 Human bac Aab16109 Human bac Aab161109 Human bac Aab11111 Human bac Aab11315 Human bac Aab11315 Human bac Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI Aab11315 Human BPI	Recomb
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	00000000000000000000000000000000000000	44 45

# ALIGNMENTS

RESULT 1 ANUC198 standard; protein; 487 AA.  XX ANUC198 standard; protein; 487 AA.  XX ANUC198; XX ANUC198; XX ANUC198; XX ANUC198; XX Human; bactericidal/permeability-increasing (BPI) protein. XX Human; bactericidal permeability-increasing protein; BPI; PMN; XX Human; bactericidal permeability-increasing protein; BPI; PMN; XX Human; bactericidal permeability-increasing protein; BPI; PMN; XX Human; bactericidal permeability-increasing protein; BPI; PMN; XX Homo sapiens. XX Homo sapiens. XX Homo sapiens. XX XX II-ANG-1989; BJUS-00309217. XX XX II-ANG-1989; BJUS-003085031. XX XX II-ANG-1989; BJUS-000805031. XX XX XX II-BC-1991; BJUS-000805031. XX XX XX XX XX XX XX XX XX XX XX XX XX
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pING4512;

pING4512 encoded fusion protein.

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The present invention relates to the isolation of human bactericidal/permeability-increasing (BPI) protein from polymorphonuclear latkocytes (PWN). BTI can be produced by growing in a culture medium, host cells transformed or transfected to express BPI encoded by chost cells transformed or transfected to express BPI encoded by cucleotides 124-1491 of the BPI polymucleotide sequence or its complementary strand. Despendent of the BPI polymucleotide sequence or its complementary strand. BPIs are useful against a wide range of Gramnegative bacteria particularly for the treatment of diseases caused by Cram-negative bacteria such as bacteraemia or sepsis, infections caused by Escherichia coli, Salmonella, Klebsiella or Pseudomonas, and skin infections which occur in bedridden patients suffering from decubitus infections which occur in bedridden patients suffering from decubitus closes) or in burn patients. They can also be used as a model for the design of new antibiotic agents, to provide sequence information on BPI to direct the design of future generations of antimicrobial agents pepcific for Cama-negative bacteria, and to be used as probes in molecular biological techniques. The presents the human BPI protein in protein therapy. The present sequence represents the human BPI protein
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Matches 487, Conservative
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Best Local Similarity 100. Matches 487; Conservative Query Match Best Local Similarity Sequence 487 AA; ò VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV 300 VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV 300 YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360 YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNWKIQIHVSASTPPHLSVQ 360 PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420 PIGLIFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420 HSNIGPPPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLF AAR44420 standard; protein; 487 AA GADVVYK 487 GADVVYK 487

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(revised)
(first entry)

25-MAR-2003 03-JUN-1994 AAR44420;

SASSES

RESULT 2 **AAR44420** 

This sequence is encoded by the plasmid pING4512. pING4512 was

constructed using the primer sequence given in AAG52480. Plasmid pINC4503

was cut with Alway. the ends made blunt with 74 DNA pOlymerase, and the
DNA then cut with Sall. The resultent approx. 700bp Sall/blunt fragment
Contains the 30 bp 5' untranslated region and the DNA encoding the signal
mains acids of bactericidal/permeability-increasing
protein (BPI). IgG heavy chain (HC) sequences, which also included the
hinge region of the IgG HC were PCR amplified from plasmid pMB27 using
these primers. Plasmids such as pING4512 may be used to produce fusion
conditions and their sequelae including endotoxin related shock and
conditions associated with it, such as disseminated intravascular
conditions anemia, thrombocytopenia, adult respiratory
distress syndrome, renal fallure, hypotension, fever and metabolic
acidosis. Proving BPI or a fragment of it, as part of the fusion with an
immunoglobulin heavy chain constant region provides the potential
cacharide complement binding and increasing placental transfer. (Updated
on 25-MAR-2003 to correct PN field.) KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG 120 KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG 120 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL 60 New fusion proteins for treating bacterial infections - comprising a bactericidal-permeability-increasing protein and a immunoglobulin heavy chain constant domain. 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISOKGLDYASQQGTAALQKEL Polymerase chain reaction; primer; amplify; PCR; plasmid; pING4512; pING4503; bactericidal/permeability-increasing protein; BPI; 1gG; heachain; pME37; fusion protein; Gram negative; renal failure; bacterial infection; endoroxin related shock; metabolic acidosis; disseminated intravascular coagulation; anemia; thrombocytopenia; leukopenia; adult respiratory distress syndrome; hypotension; fever; constant region; lipopolysaccharide complement binding; placental transfer; PC receptor binding. Gaps ó, Length 487; /note= "Mature rBPI(191)-IgG fusion protein" Indels 4.3e-229; DB 100.0%; Score 2507; 100.0%; Pred. No. 4.3 iive 0; Mismatches l. .31 /note= "Signal peptide" Claim 20; Page 48-50; 75pp; English. Location/Qualifiers Horwitz A; 93WO-US004754. 92US-00885911 .487 Grinna LS, WPI; 1993-386485/48. N-PSDB; AAQ52488. (XOMA ) XOMA CORP. WO9323434-A2 19-MAY-1993; 19-MAY-1992; 25-NOV-1993 Theofan G, Synthetic 61 Peptide Protein 쉱 g ò

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us-10-629-516-2.rag

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This sequence represents the N-terminal of recombinant bactericidal/permeability (rBPI) protein. This expression product encoding the 31 residue signal protein and the first 199 amino acids of the N-terminal of mature human BPI has a molecular weight of 23 kD and is designated rBPI-33. In binding assays rBPI-23 was shown to have three separate functional domains with heparin-binding activity, at least three major domains with significant Limulus amcebocyte lysate (IAL) inhibition and one region with bactericidal activity. BPI, or active fragments of it may be used to treat and prevent the effects of chronic inflammatory disease states such as arthritis, psoriasis, inflammatory bowel disease, Crohn's disease and asthma. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                             Uses of bactericidal permeability increasing protein product - to neutralise anticoagulant effect of heparin, to inhibit angiogensis cell proliferation, as contraceptive and to reduce inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2507; DB 2;
100.0%; Pred. No. 4.3e-229;
ive 0; Mismatches 0;
                                                                                                        Parent JB;
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Best Local Similarity 100.0%;
Matches 487; Conservative (
94WO-US002401
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11-MAR-1994;
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                                                                                                                                                     N-terminal; recombinant; bactericidal/permeability protein; rBPI; signal protein; human; rBPI-23; binding assay; heparin-binding; domain; Limulus amoebocyte lysate; LAL; inhibition; bactericidal activity; chronic inflammatory disease; arthritis; psoriasis; Crohn's disease; inflammatory bowel disease; asthma.
                                                                                            YQEAGVLKMTLRDDMI PKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                                                                                                                                                                                                                                                                  KWKAQKRFLKMSGNPDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                                                      VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV
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                                                                          KVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant bactericidal/permeability-increasing protein (rBPI-50)
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/note= "LAL inhibiting domain"
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ce= "Heparin binding site"
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/note= "7
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/note= "H
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Length 487; Indels 9 9 180 180 240 240 300 300 360

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Treating Mycobacterium infections with bactericidal-permeability inducing peptide - also used for in vivo and in vitro neutralisation of mycobacterial lipoarabinomannan.
                    301 YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                         YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR62344 shows the recombinant 23 kD, 199 amino acid residue aminoterminal fragment of human BPI (bactericidal/permeability-increasing protein) holoprorein referred to as rBPI23. The sequence given is taken from Grey et al., and varies to that from Gazano-Santoro et al. In the latter, the valine at position 141 is specified by GTG rather than GTC and residue 185 is glutemaic acid (specified by GAG) rather than Iysine (specified by AAG). The expression vector also encodes for a 31 residue signal sequence. rBPI23 or biologically active derivs. are useful in the treating of a subject suffering from any of the physiological effects of LAM (lipoarabinomannan) from Mycobacteria. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                             421 HSNIGPPPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLF
                                                                      361 PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK
                                                                                                                                                                    421 HSNIGPFPVELLQDIMMYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BPI; bactericidal/permeability-increasing protein; rBPI23; therapy; treatment; infection; Mycobacteria; leprosy; tuberculosis; LAM; lipoarabinomannan; improved pulmonary clearance; gram negative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32. 487 ____/label= N-terminus_ of_human_BPI_holoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant 23 kD human BPI N-terminal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .31
/label=_signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 21-23; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     AAR62344 standard; protein; 487 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-302680/37.
                                                                                                                                                                                                                       481 GADVVYK 487
                                                                                                                                                                                                                                                         481 GADVVYK 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ72017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumonia model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XOMA ) XOMA
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02-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lambert LH;
   301
                                                                                                                                                                                                                                                                                                                                                                                         AAR62344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVDNVGLKFSISNANIKISG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bactericidal permeability-increasing protein analogues with Cys132 or Cys135 replaced - also fusion proteins and C-terminally truncated forms, have increased stability and are useful to treat gram-negative bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPI are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQGGTAALQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVGWLIQLFHKKIESALRNKANSQVCEKVTNSVSSKLQPYFQTLPVATKIDSVAGINYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analogs, fusion proteins and C-terminal truncated forms of human claimed that show improved resistance to dimerization and adduct formation. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                       BPI; bactericidal-permeability-increasing protein; bactericide;
fusion protein; Gram-negative bacterium; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2507; DB 2; Length 487; 100.0%; Pred. No. 4.3e-229; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grinna L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baltaian M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 52-54; 77pp; English.
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      1. .31
/label= Sig_peptide
                                                         standard; protein; 487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US001235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-00013801
                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theofan G, Horwitz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-279744/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ67270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 487 AA;
                                                                                                                                                                                       Bactericide BPI
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                           WO9418323-A1
                                                                                                                               25-MAR-2003
29-MAR-1995
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                                                         AAR57901
                                                                                             AAR57901;
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Best Local S
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VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV 300
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                                                                                              binding protein deriv. and hybrid protein binds to lipo:polysaccharide lacks CD14-mediated immuno:stimulatory properties, used to treat Gramnegative bacterial infections and associated conditions.
                                                                                                                                                                                              increasing protein (rBPI). The protein contains the lipopolysaccharide (LPS) binding domain fragments described in ARR68919-R68921. The fragments are used in the construction. of hybrid proteins for the treatment gram-negative bacterial infections and associated conditions. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 HSNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLFTPARVQLYNVVLQPHQNFLLF
                                                                                                                                                                                                                                                                                                                                                                                            1 MRENWARGPCNAPRWYSLAVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                   KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVGWLIQLFHKKIESALRNKANSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YQEAGVLKMTLRDDMI PKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK
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                                                                                                                                                                                                                                                                                                                                                                           1 MRENMARGPCNAPRWVSLMVIVAIGTAVTAAVNPGVVVRISOKGLDYASQQGTAALQKEL
                                                                                                                                                                                    encodes AAR68923 recombinant bactericidal/permiability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant bactericidal/permeability-increasing protein rBPI.
                                                                                                                                                                                                                                                                                                                    487;
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                  100.0%; Score 2507; DB 2;
100.0%; Pred. No. 4.3e-229;
ive 0; Mismatches 0;
                            PW;
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                                                                                                                                                          Example 2; Page 70-72; 114pp; English
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                                                       WPI; 1995-052078/07
N-PSDB; AAQ80827.
                                                                                                                                                                                                                                                                                                                                 Similarity
                            Gazzano-Santoro H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GADVVYK
(XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GADVVYK
                                                                                                                                                                                                                                                                                         Sequence 487 AA;
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21-DEC-1995
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Best Local Simi
Matches 487;
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                                                                                                                                                                                                                                                                                            VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV 300
                                                                                                                                                                                                                                                                                                                                                  YOEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                                                                                                                                                                                                                                                                                                                                            YOEAGVLKMTLRDDMI PKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSNIGPFPVELLQDIMNYIVPILVLPRVNEXLQKGFPLPTPARVQLYNVVLQPHQNFLLF 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG 120
                                                                                                                                                                                                                    KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180
                                                                                                                            9
                                                                                                                                                                                                                                   KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                                   1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                                                                                                                                                                                                                                                          KVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
                                                                        Gaps
                                                                      ö
                                           487;
                                          Length
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bactericidal/permeability-increasing protein (rBPI)
                                          Score 2507; DB 2;
Pred. No. 4.3e-229;
                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipopolysaccharide binding protein; rLPB; LPS; gram-negative bacterial infections; treatment; bactericidal/permeability-increasing protein.
                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l. .32
/label= sig_peptide
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                                          100.0%;
100.0%;
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                                                                         Conservative
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                                                          Local Similarity
nes 487; Conserv
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                  Sequence 487
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11-SEP-1995
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                                             Query Match
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Recombinant endotoxin-binding protein comprising bactericidal/permeability increasing protein (BPIP) or its endotoxin N-terminal fragment, can be produced by growing genetically transformed host cells in a suitable medium so that BPIP is secreted into the medium. The BPIP is then isolated and can be used to control bacterial infections. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recovery of recombinant endotoxin binding protein - by culturing transformed cells in medium contg. cation exchange material, useful for treatment of bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bactericidal permeability increasing protein; BPIP; infection; control; recombinant.
                                                                                                         241 VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVXLGLSDYFFNTAGLV
                                                                                                                                                                                         301 YQEAGYLKWILRDDMIPKESKFRLTTKFPGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                                                                                                                                                                                                                                                                                                                                                      421 HSNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLF
                                                                                                                                                               YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                                                                                                                                                                                                                                        PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bactericidal/permeability increasing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Col 13-16; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endotoxin in circulation. BPI protein products are administered in dosagants. of 0.1-10 mg/kg body wt. by parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENWARGPCNAPRWYSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of humans exposed to bacterial endotoxin in circulation - bactericidal/permeability-increasing protein product to alleviate increase in circulating tumour necrosis factor and interleukin 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Von Der Mohlen MAM;
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                       Bactericidal/permeability-increasing protein; BPI; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Deventer SJH,
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                                                                                                                                          Location/Qualifiers
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/label= signal
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94US-00291112
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                                                   Gram negative bacteria.
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                                                                                                  Homo sapiens
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16-AUG-1994;
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Scannon PJ,

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WPI; 1995-263713/34
Lim E,
                         N-PSDB; AAQ99816
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Little RG,
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                                                   KRIKI PDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQI SMVPNVGLKFSI SNANIKI SG
                                                                                     KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                                       VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV
                                                                                                                                                                                   YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                                                                                                                                                                          VQEAGVLKATLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                                                                                                                                                                                                               HSNIGBFFVELLQDIMYYIVPILVLPRVNEKLQKGFFLPTPARVQLYNVVLQPHQNFLLF
                         MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                          KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG
                                                                           KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                               KVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
                                                                                                                                               VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV
                                                                                                                                                                                                                     PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLLELK
                                                                                                                                                                                                                                                       HSNIGPFPVELLQDIMNYIVPILVLPRVNEXLQKGFPLPTPARVQLYNVVLQPHQNFLLF
                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant bactericidal/permeability increasing holoprotein.
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/note= "mature peptide"
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94US-00209762.
94US-00273540.
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/note= '
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11-MAR-1994;
11-JUL-1994;
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Peptide
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The amino acid sequence of a recombinant bactericidal/permeability increasing (BPI) protein. BPI protein can be isolated from the granules of mammalian polyworphonuclear neutrophils (PMN). The protein has antibacterial activity associated with 3 functional domains: I (AAR81085), II (AAR81086) and III (AAR81087) present in N-terminal region of the BPI holoprotein (AAR81245). The antibacterial regions were used to design the antifungal peptides AAR81081, AAR81088-R81244 and AAR81248-R81308. The peptides are used to treat fungal infections together with other antifungal cpds e.g. fluconazole or amphotericin B. The antifungal activity of the peptides may also be enhanced by addition of a nipopolysaccharide binding protein (LBP) e.g. AAR81246. The peptides can be used to treat fungal infection, esp. Candida albicans. They are also useful for killing or inhibiting fungi in vitro e.g. for sterilising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPBVAKKFPNMKIQIHVSASTPPHLSVQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
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Treating fungal infection with bactericidal permeability increasing protein or deriv. - esp. for control of systemic Candida albicans infection or for use in in vitro sterilisation.
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100.0%; Pred. No. 4.3e-229;
iive 0; Mismatches 0;
                                                                                                                                  Example 1; Page 105-107; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR80995 standard; protein; 487 AA
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                      241 VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV
                                                                     YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV
                                                                                                                                             PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bactericidal/permeability-increasing protein; BPI; rBPI; rBPI50; lipopolysaccharide binding protein; LBP; rLBP25; rLBP; Gram-negative bacterium; infection; antiseptic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for treating gram negative bacterial infection - administering lipopolysaccharide binding protein (LBP) pactericidal/permeability-increasing (BPI) protein prod
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/label= Mat_peptide
/note= "rBPI50 holoprotein"
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/label= Sig_peptide
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94US-00274303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide(s) based on bactericidal/permeability-increasing protein -
having heparin binding and neutralisation, LPS binding and neutralisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant bactericidal/permeability increasing protein (rBDI) is encoded by AAT00951. BPI (bactericidal permeability-increasing) peptides (AAR80996-81081 and AAR8255-372) each have an amino acid sequence that is deriv. of a BPI functional domain (or a variant) having at least one of the biological activities of BPI, such as heparin binding or neutralisation, lipopolysaccharide (LPS) binding or neutralisation or bactericidal activity. The BPI peptides are based on the amino-terminal portion of BPI, esp. functional domains I, II, and III (BPI residues 17-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRENWARGPCNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL 60
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                                                                                                         bactericidal/permeability increasing peptide; BPI; heparin; binding; neutralisation; lipopolysacchaide; LPS; bactericidal activity; treatment; neutralise endotoxin; inhibit angiogenesis; inhibit tumour formation; proliferation.
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                                                                           Bactericidal/permeability increasing protein (rBPI).
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                                                                                                                                                                                                                                                          1. .31
/label= Signal_peptide
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/label= mature_peptide
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94US-00209762
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N-PSDB; AAT00951.
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                                          MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISOKGLDYASOQGTAALQKEL
                                                     KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG
                                                                                                             KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
                                                                                                                                              KVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
                                                                                                                                                                               VAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLV
                                                                                                                                                                                                                  YQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
                                                                                                                                                                                                                                                    PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK
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                         Gaps
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         Length 487;
                        Indels
        100.0%; Score 2507; DB 2;
100.0%; Pred. No. 4.3e-229;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      for use in treating liver damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
32. .487
/label= rBPI
                                                                                                                                                                                                                                                                                                                                                                                   AAR86455 standard; protein; 487 AA.
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                 Local Similarity 100.
nes 487; Conservative
                                                                                                                                                                                                                                                                                                                                         487
                                                                                                                                                                                                                                                                                                                       GADVVYK 487
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                                                                                                                                                                                                                                                                                                                                    GADVVYK
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         Query Match
Best Local Si
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                                          Use of bactericidal/permeability-increasing protein prods. - for treating adverse physiological effects of a depressed reticuloendothelial system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                    adverse effects associated with depressed reticuloendothelial system function, especially diminished function of Kupfer cells of the liver resulting from physical, chemical or biological insult. Physical insult is exemplified by partial or total hepatectomy such as accompanies transplantation, and trauma. Chemical insult is exemplified by the results of exposure to hepatectoxic substrances such as chloroform, glucosamine, carbon tetrachloride and ethanol. Biological insult is exemplified by (non-)infectious diseases such as viral hepatitis and enfancing inflammantory hepatitis. The BPI protein product is preferably rBPI-21, rBPI, rBPI, rBPI-42 dimer or one of 222 specified BPI peptides. The present sequence is that of rBPI
                                                                                                                                                                                  patent relates to the new use of a BPI protein product for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPUVGLKFSISNANIKISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQEAGVLKMTLRDDMI PKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ
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                                                                                                                                        Claim 6, 13; Page 42, 43; 136pp; English
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1995-161572/21
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This is the amino acid sequence of a bactericidal/permeability increasing (BPI) protein. BPI is a protein isolated from the granules of mammalian polyworphomuclear leukocytes. It is a 55 kD cationic protein which has potent antibacterial activity against a broad range of Gram -ve bacteria. The sequence was used to generate the peptides (AAM05853-W06074) which were screened for bactericidal activity against E.coli strains US and 0111:B4 in a radial diffusion assay. The BPI peptides can be used to enhance the treatment of Gram -ve bacterial infections, prophylactically for patients about to undergo surgery or for disinfection or sterilisation. Administration of the BPI peptides together with an antibiotic results in synergistic or potentiating bactericidal effects greater than the effect of the individual peptide or antibiotic. Also the BPI peptides can reverse the resistance of certain Gram -ve bacteria to certain antibiotics e.g. carbenicillin, cefazolin. (Updated on 25-MAR-
                420
                                    361 PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
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                                                                                                              PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK
                                                                                          HSNIGPPPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipopolysaccharide binding protein; synergist; BPI; enhancement; bactericidal/permeability increasing protein; potentiation; surgery; Gram negative; bacterial infections; disinfection; sterilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic; E.coli; polymorphonuclear leukocyte; mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant bactericidal/permeability increasing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mature recombinant BPI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
32. .487
/note= "mature recombine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The recombinant BPI (bacterial permeability-increasing), is designated rBPI23. BPI peptides (AAR76244-458) were screened for bactericidal effects on B. coli strains J5 and 011:184 in a radial diffusion assay. BPI peptides which retain antibacterial activity are expected to improve the therapeutic effectiveness of antibiotics when concurrently administered. Concurrent administration of BPI protein products and antibiotics is shown to reverse resistance of a variety of gram-negative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPI protein and an antibiotic in a medicament - for treatment of gramnegative bacterial infection.
                                  BPI peptide; bacterial permeability-increasing peptide; bactericidal; therapeutic effectiveness; antibiotic; concurrent administration; reverse resistance; gram-negative bacteria.
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100.0%; Pred. No. 4.3e-229;
iive 0; Mismatches 0;
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/note= "mature recombinant BPI"
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                                                                                                                                                                         1. .31
/note= "signal peptide"
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94US-00273401
Recombinant BPI holoprotein.
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N-PSDB; AAQ92640.
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11-JUL-1994;
                                                                                                                Homo sapiens
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13-JAN-1995;
19-SEP-1995;
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                                                                                                                                                            PIGLIFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK
                                                           MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                                                                                          KRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISG
                                                                                                                       KWKAQKRFLKMSGNFDLS1EGMS1SADLKLGSNPTSGKPT1TCSSCSSHINSVHVH1SKS
                                                                                                                                                    KVGWLIQLFHKKI ESALRNKMNSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYGL
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                                            Gaps
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                               Length 487;
                                            Indels
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                             Query Match
100.0%; Score 2507; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.3e-229.
Matches 487; Conservative 0; Mismatches 0;
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                Sequence 487 AA
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                                            Compsn. comprising bactericidal permeability increasing protein prod. and bactericidal activity enhancing poloxamer surfactant - useful for treating bacterial infections, and for inhibiting bacterial and fungal growth.
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                                                                                                                                                                                                                                            The known anti-microbial properties of bactericidal/permeability increasing protein (BPI) can be enhanced by administering the BPI with a stabilising polyoxypropylene-polyoxyethylene block copolymer (poloxamer). Therapeutic compositions pref. contain one of the poloxamers 333, 334, 335 or 403 and opt. comprise EDTA. They are useful for treating bacterial and fungal infections. The present sequence is that of human recombinant BPI and was disclosed in Gray et al., J.Biol.Chem., 264:9505 (1989)
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100.0%; Pred. No. 4.3e-229;
ive 0; Mismatches 0;
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WPI; 1996-342029/34.
N-PSDB; AAT31853.
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Sequence 2 Sequence 2 Sequence 6

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US-09-782-642-2 US-09-255-245-2 US-09-861-198A-2 US-09-861-400-15 US-09-861-400-15 US-09-861-400-15 US-09-861-400-15 US-09-975-638B-3 US-09-975-638B-3 US-09-975-638B-3 US-09-975-638B-3 US-09-975-638B-3 US-09-975-638B-3 US-10-128-139-2 US-10-128-139-2 US-10-136-646-2 US-10-136-646-2 US-10-136-646-2 US-10-136-646-2 US-10-136-646-2 US-10-34-163A-2 US-10-34-163A-2 US-10-299-985-2 US-10-299-985-2 US-10-299-985-2 US-10-299-985-2 US-10-299-985-2 US-10-299-985-2 US-10-446-628-146 US-10-399-985-2 US-10-399-985-2 US-10-399-985-2 US-10-139-013-139 US-10-139-013-139 US-10-471-1153 US-10-473-127-1154

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ALIGNMENTS

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US-09-759-100B-408

Sequence 408, Application US/09759130B

Sequence 408, Application US/09759130B

Sequence 408, Application No. US2030022279A1

GENERAL INFORMATION:

APPLICANT: Milennium Pharmaceuticals, Inc.

APPLICANT: Barnes, Thomas S

APPLICANT: Barnes, Thomas S

APPLICANT: Barnes, Thomas S

APPLICANT: Mackay, Charles R

APPLICANT: Mackay, Charles R

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APPLICANT: Mackay, Charles R

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APPLICANT: Mackay, Charles R

APPLICANT: Mackay, Charles R

APPLICANT: Wighton, Nicolas

APPLICANT: Wighton, Nicolas

APPLICANT: Wighton, Nouglas A

TITLE OF INVENTION: WOWEL GENES ENCODING PROTEINS HAVING

TITLE REFERENCE: MPHOD-5350NMIN

TITLE REPRENCE: MPHOD-5350NMIN

TITLE REPRENCE: MPHOD-5350NMIN

CURRENT APPLICATION NUMBER: US 09/559, 497

PRIOR PILING DATE: 2000-01-07

PRIOR FILING DATE: 2000-01-07

PRIOR PILING DATE: 2000-01-07

PRIOR FILING DATE: 2000-01-07

PRIOR FILING DATE: UNMBER: US 09/559, 194

PRIOR FILING DATE: UNMBER: US 09/596, 194

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14
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 Sequence 408, App
Sequence 38, Appl
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Sequence 265, App
Sequence 26, Appl
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US-09-765-527-265
US-09-760-397-16
US-09-881-490-206
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66 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 125
                                                                    121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
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APPLICANT: MCCARTHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: MOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REPERENCE: 10147-6U2
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 38
LENGTH: A.83
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 943; DB 10;
100.0%; Pred. No. 3.4e-84;
iive 0; Mismatches 0;
  PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SEQ ID NO 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 38, Application US/10042431; Publication No. US20020182675A1; GENERAL INFORMATION:
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Matches 184; Conservative
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ORGANISM: Homo Bapiens
US-10-042-431-38
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ORGANISM: Homo sapiens
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181 HKKI 184
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US-09-765-527-265
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                                                         126 KASGNPDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 185
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DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 125
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Sequence 1241, Application US/10473127
Fublication No. US20040236091A1
GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION UNMBER: US/10/473,127
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR PILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR APPLICATION NUMBER: 60/10,801
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2002-02-04
SPRIOR FILING DATE: 2002-02-05
NUMBER OF SEC ID NOS: 2041
SOFTWARE: FARESQ for Windows Version 4.0
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ORGANISM: Homo sapiens
US-10-473-127-1170
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DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago.
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COUNTRY: United States of America
ZIP: 66060-6400
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
ATTONER/APPLICATION NUMBER: 08/621,803
ATTONER/APPLICATION NUMBER: 25,447
REGISTRATION NUMBER: 25,447
REGISTRATION NUMBER: 25,447
TELECOMMUNICATION: NUMBER: 25,447
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR PILING DATE: 2001-10-01
PRIOR PRILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2002-02.20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FRACESQ for Windows Version 4.0
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Best Local Similarity 100.0%;
Matches 184; Conservative
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RESULT 8
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Sequence 16, Application US/09760397

Fatent No. US20020009781A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Gavit, Patrick D.

TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production

FILE REFERENCE: 1103/11041US01

CURRENT APPLICATION NUMBER: 103/09/760,397

CURRENT FILING DATE: 2001-01-12

FRIOR APPLICATION NUMBER: 09/271,970

FRIOR PILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                      1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
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100.0%; Pred. No. 3.5e-84;
iive 0; Mismatches 0;
                                                                                                                                                                                                                        100.0%; Score 943; DB 9; 100.0%; Pred. No. 3.5e-84;
                                                                                                                                                                                                                                                                0; Mismatches
                                                                                    TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-765-527-265
              INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TELEFAX: 312/474-0448
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Best Local Similarity
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Best Local Similarity
Matches 184; Conserv
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ORGANISM: Human
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LENGTH: 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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                                                                                                                                          TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive CITY: Chicago
STATE: 1111nois
COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MCNIGOLOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
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Matches 184; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,490
FILING DATE: 14-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPELCATION UNMERS: 09/119,858
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/372,105
FILING DATE: 13.4AN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15.5EP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11.4UL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11.4MR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14.4AN-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14.4AN-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14.4AN-94
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-881-490-206
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
                     Sequence 206, Application US/09881490 Patent No. US20020077298A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                  APPLICANT: Little II, Roger G. Lim, Edward
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SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
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TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60661
COMPUTER READABLE FORM:
JS-09-881-490-206
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130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Therapeutic Uses of BPI Protein Products NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 KWSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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COMPUTER: 111inois
COUNTRY: United States of America
ZIP: 6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/733,613
FILING DATE: 08-Dec-2000
CLASSIFICATION NUMBER: 09/388,758
FILING DATE: 1999-00-02
ATTORNEY/AGENI INFORMATION:
NAME: Michael F. Borun
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 25,447
TELEROMINICATION INDREMATION:
TELEROMINICATION INDREME: 21,474-6300
TELEROMINICATION INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 3.5e-84;
Matches 184; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   Scannon, Patrick J.
van Deventer, Sander J.H.
von der Mohlen, Marijke A.M.
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
                                                                                                                                                                                                                                                              Sequence 2, Application US/09733613
Patent No. US20020094952A1
GENERAL INFORMATION:
APPLICANT: Friedmann, Nadav
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                                                             181 HKKI 184
                                                                                                                    190 HKKI 193
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130 KASGNFDLSIEGASISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGML1QLF 189
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                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09942021
Patent No. US20020090368A1
GENERAL INPORMATION:
APPLICANT: Little, Roger G. II
APPLICANT: Little, Roger G. II
IITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability
Increasing (BPI) Protein Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/942,021
FILING DATE: 27-Aug-2001
CLASSIFICATION: AUMBER: US/200,427
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: 09/220,427
FILING DATE: March 31, 1995
APPLICATION NUMBER: 08/415,158
FILING DATE: March 12, 1993
APPLICATION NUMBER: 08/030,644
FILING DATE: Warch 12, 1993
APPLICATION NUMBER: 08/030,644
FILING DATE: March 12, 1993
APPLICATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11004US07 / 100-224.P1.C3
TELECOMMUTCATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: MCANATews, Held & Malloy, Ltd. STREET: 500 W. Madison Street, 34th Floor CITY: Chicago STATE: 111inois COUNTRY: USA
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Pred. No. 3.5e-84;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/707-9155
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60661
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 184; Conservative
                                                                                                                                                      190 HKKI 193
                                                                                               HKKI 184
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                                                                                                                                                                                                                                               RESULT 9
US-09-942-021-2
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US-09-782-642-2
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                                                                                                                                                                                                   Uses of BPI Protein Products
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 943; DB 9; Length 487; 100.0%; Pred. No. 3.5e-84;
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEADELS SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,938
APPLICATION DATA:
APPLICATION NUMBER: US/09/365,858
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: US/09/365,858
FILING DATE: CUNKNOWN-
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
RECISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 27129/33248
TELEPHONE: 212/474.6300
                                                                                                                                                                          Scannon, Patrick J.
TITLE OF INVENTION: Therapeutic Uses of BPI Pr
for Human Meningococcemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                        STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-728-938-2
                                                                                               ; Sequence 2, Application US/09728938
; Patent No. US20020103114A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 487 amino acids
                                                                                                                                                          APPLICANT: Giroir, Brett P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606-6402
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                          RESULT 11
US-09-728-938-2
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RESULT 12

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70 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVFNVGLKFSISNANIKISGKWKAQKRFL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 KASGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGMLIQLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSFKIKHLGKGHYSFYSMDIRBFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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100.0%; Score 943; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.5e-84;
Matches 184; Conservative 0; Mismatches 0; Indels
                                                                                                     Treatment of Mycobacterial Diseases
by Administration of
Bactericidal/Permeability-Increasing
                                                                                                                                                                                                                                                                                                                       6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,642
FILING DATE: 13-Feb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/626,646
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFFERENCE/DOCKET NUMBER: 31293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                       Protein Product
                                                                               APPLICANT: Lewis H. Lambert, Jr. TITLE OF INVENTION: Treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
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; Sequence 2, Application US/09255245
; Patent No. US20020119918A1
; GENERAL INFORMATION:
Sequence 2, Application US/09782642 Patent No. US20020103118A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 487 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                Chicago
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Sequence 2, Application US/09866514

Sequence 2, Application US/09866514

Sequence 2, Application US/09866514

GENERAL INFORMATION: THERAPEUTIC USES OF BACTERICIDAL/PERMEABILITY-INCREASING

TITLE OF INVENTION: THERAPEUTIC USES OF BACTERICIDAL/PERMEABILITY-INCREASING

TITLE OF INVENTION: PROTEIN FRAGMENTS

FILE REFERENCE: 28297/32248B

CURRENT APPLICATION NUMBER: 08/98/866,514

CURRENT FILING DATE: 1999-05-10

FRIOR APPLICATION NUMBER: 09/309,217

FRIOR APPLICATION NUMBER: 09/309,217

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATCHIN Ver. 2.0

SEQ ID NO 2

TENGRAL APPLICATION OF SEQ ID NOS: 6

SEQ ID NO 2

TENGRAL APPLICATION OF SEQ ID NOS: 6

SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CNAPRWYSLMYLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 943; DB 9; Length 487; 100.0%; Pred. No. 3.5e-84; ive 0; Mismatches 0; Indels (
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: DatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/941,198A
FILING DATE: 27-Aug-2001
CLASSIFICATION *CURROWN>
PRIOR APPLICATION *CURROWN>
PRIOR APPLICATION NUMBER: 08/557,289
FILING DATE: *CURROWN>
ATORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE DOCKET VUNBER: 25,447
FELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
6300 Sears Tower, 233 South Wacker Drive
                      CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HKKI 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69
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                          THERAPEUTIC USES OF N-TERMINAL BPI PROTEIN PRODUCTS IN ANCA-POSITIVE PATIENTS
                                                               NUMBER OF INVENTION:

NUMBER OF SEQUENCES: 2

CORRESPONDENCES: 2

CORRESPONDENCES: 4

CORRESPONDENCES: 4

CITY: 6100 Scars Tower, 233 South Wacker Drive

CITY: Chicago
STATE: 111inois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER FABABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Nelease #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/255,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 487;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
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Patent No. US20020128191A1

GENERAL INPORMATION:

APPLICANT: Scannon, Patrick J.

TITLE OF INVENTION: METHODS OF TREATING CONDITIONS
ASSOCIATED WITH CORNEAL INJURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 943; DB 9;
100.0%; Pred. No. 3.5e-84;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/742,985
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 2712
TELECOMMUNICATION INFORMATION:
TELECHONE: 312/474-6300
TELEFAX: 312/474-6448
       Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
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amino acid
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Best Local Similarity 100.
Matches 184; Conservative
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                          TITLE OF INVENTION:
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Query Match 100.0%; Score 943; DB 9; Length 487; Best Local Similarity 100.0%; Pred. No. 3.5e-84; Matches 184; Conservative 0; Mismatches 0; Indels 0
; ORGANISM: Homo sapiens
US-09-866-514-2
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0; Gaps

61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFL 120 	121 KMSGNFDLSTEGMSTSADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLF 180	130 KMSGNFDLSIEGMSISADLKLGSNFTSGKFTITCSSCSSHINSVHVHISKSKVGWLIQLF 189	181 HKKI 184	190 HKKI 193
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Search completed: October 21, 2005, 11:37:02 Job time : 65.7154 secs

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Sequence 16, Appl
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                                                                                                                October 21, 2005, 11:22:45 ; Search time 171.285 Seconds (without alignments) 1187.019 Million cell updates/sec
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2507
1 MRENMARGPCNAPRWVSLMV........nVVLQPHQNFLLFGADVVYK 487
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| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB. pep:*
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22: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB. pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-760-397-16
US-09-981-490-206
US-09-942-021-2
US-09-733-613-2
US-09-733-613-2
US-09-733-642-2
US-09-255-245-2
US-09-941-198A-2
US-09-866-514-2
US-09-861-400-15
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                                                                                                                                                                                                                                                                                                                                             1862951 seqs, 417491010 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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No.
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ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:

ATTORNEY AND MUMBER: 08/621,803
PILING DATE: 4Unknown:
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:

TELEFAX: 312/474-0448

equence 2, equence 3, equence 2, equence 2, equence 2, equence 2, equence 2, equence 2, equence 2,	Sequence 28, Appl Sequence 18, Appl Sequence 16, Appl Sequence 16, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 69, Appl Sequence 115, Appl Sequence 1151, Appl Sequence 1153, Appl Sequence 1153, Appl Sequence 1153, Appl Sequence 1154, Appl Sequence 1155, Appl Sequence 1155, Appl Sequence 1155, Appl Sequence 1155, Appl Sequence 1155, Appl Sequence 1155, Appl Sequence 1155, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Seq	1159, 1160, 1161, 1163, 1163,	Microbial Production of -Derived Peptides , Murray & Borun cker Drive
US-09-746-311-2 US-09-975-638B-3 US-09-416-828-2 US-09-480-234-2 US-10-006-557-2 US-10-226-810-2 US-10-128-139-2 US-10-196-460-2	US-10-146-126-2 US-10-209-611-28 US-10-131-686A-12 US-10-342-169A-2 US-10-299-985-2 US-10-299-985-2 US-10-299-985-2 US-10-296-2 US-10-16-186-69 US-10-446-628-146 US-10-446-628-146 US-10-446-639-146 US-10-446-639-146 US-10-446-639-146 US-10-446-639-146 US-10-446-639-146 US-10-473-127-1151 US-10-473-127-1155 US-10-473-127-1155 US-10-473-127-1155 US-10-473-127-1155	10-473-127-115 10-473-127-115 10-473-127-116 10-473-127-116 10-473-127-116	765527  D.  ods for Recombinant on Proteins and BPI- , O'Toole, Gerstein, Tower, 233 South Wac
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25507 25507 25507 25507 25507 25507	2507 2507 2507 2507 2507 2507 2507 2507		SULT 15-265 -09-765-527-265 Sequence 265, App Patent No. US200 GENERAL INFORM APPLICANT TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
TILE OF INVENTION: Improved Methods for Recombinant Peptide Production FILE OF INVENTION: Improved Methods for Recombinant Peptide Production FILE REFERENCE: 1103/11041US01
CURRENT APPLICATION NUMBER: US/09/760,397
CURRENT FILING DATE: 2001-01-12
PRIOR RAPLICATION NUMBER: 09/271,970
PRIOR PILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                Length 487;
                                                                                                                                                                           Indels
                                                                                                                                             100.0%; Score 2507; DB 9;
100.0%; Pred. No. 1.7e-209;
tive 0; Mismatches 0;
                              LENGTH: 487 amino acids
LENGTH: 487 amino acids
TYPE: amino acid
TYPE: protein
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-765-527-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 16, Application US/09760397; Patent No. US20020009781A1; GENERAL INFORMATION:
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 487; Conservative
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ORGANISM: Human
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DB 9; Length 487;

100.0%; Score 2507;

Query Match

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                                                                                                              1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
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                                                                    MRENMARGPCNAPRWVSL,MVL,VAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKEL
                       Gaps
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STREET: 500 West Madison Street, 34th Floorbrive
CITY: Closego
STATE: 111inois
COUNTRY: United States of America
                       Indels
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Pred. No. 1.7e-209; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim, Edward
Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/881,490 FILING DATE: 14-Jun-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/119,858
FILING DATE: 4Unknown-
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 206, Application US/09881490; Patent No. US20020077298A1; GENERAL INFORMATION:
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al Similarity 100.0%; P. 487; Conservative 0;
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Best Local Similarity
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NAME: MCNIGOLDAS, Janet M.
REGISTRATION NUMBER: 32, 918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 2507; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0;
                APPLICATION NUMBER: 08/209,762
FILING DATE: 11-WAR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-0AN-94
APPLICATION NUMBER: 08/093,202
FILING DATE: 12-UD-93
APPLICATION NUMBER: 08/093,644
FILING DATE: 12-MAR-93
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-881-490-206
FILING DATE: 11-JUL-94
ADDI.TCATION NUMBER: 08/209,762
                                                                                                                                                                               TELECOMMUNICATION INFORMATION
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                  LENGTH: 487 amino acids
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INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               TYPE: amino acid
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US-09-942-021-2
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APPLICANT: Little, Roger G. II

Sequence 2, Application US/09942021 Patent No. US20020090368A1 GENERAL INFORMATION:

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KWKAQKRFLKWSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180
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TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability Increasing (BPI) Protein Products
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                                                                                                                                                                Indels
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100.0%; Pred. No. 1.7e-209;
ative 0; Mismatches 0;
                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
                                                                                                                             ZIP: 60661
COMPUTER READABLE FORM:
                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 487; Conservative
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TOPOLOGY: linear
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US-09-728-938-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 HSNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLF 480
                                     PIGLIFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
PTGLTFYPAVDVQAFAVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELK 420
                                                                                                                             HSNIGPFPVELLQDIMNYIVPILVLPRVNEKLOKGFPLPTPARVQLYNVVLQPHONFLLF 480
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INVENTION: Human Therapeutic Uses of BPI Protein Products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/733,613
FILING DATE: 08-Dec-2000
CLASSIFCATION SYMENDER: US/09/733,613
FILING DATE: 08-Dec-2000
CLASSIFCATION DATA:
PRIOR APPLICATION DATA:
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FILING DATE: 1999-02
ATTORNEY/AGENT INFORMATION:
NAME: Michael F. Borun
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/32451
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scannon, Patrick J.
van Deventer, Sander J.H.
von der Mohlen, Marijke A.M.
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-733-613-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09733613
Patent No. US20020094952A1
GENERAL INFORMATION:
APPLICANT: Friedmann, Nadav
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CORRESPONDENCE ADDRESS:
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Matches 487; Conserva
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KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS 180
                            121 KWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKS
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Scannon, Patrick J.
TITLE OF INVENTION: Therapeutic Uses of BPI Protein Products
for Human Meningococcemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/365,858
FILING DATE: cunknown>
FILING DATE: cunknown>
FILING DATE: cunknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, ufefrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 27129/33248
TELECOMMUNICATION INFORMATION:
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STATE: 1111nois
COUNTY: United States of America
ZIP: 60606-6402
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/728,938
FILING DATE: 30-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09728938 Patent No. US20020103114A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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US-09-255-245-2
Sequence 2, Application US/09255245
Sequence 2, Application US/09255245
SENERAL INFORMATION:
APPLICANT: "*Carroll, Stephen F.
TITLE OF INVENTION: THERAPEUTIC USES OF N-TERMINAL BPI ITLE OF INVENTION: PRODUCTS IN ANCA-POSITIVE PATIENTS
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Boru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2507; DB 9; 100.0%; Pred. No. 1.7e-209;
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                                                                                                                         REFERENCE/DOCKET NUMBER: 35,447
REFERENCE/DOCKET NUMBER: 31293
TELEPOMNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEFAX: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                          NAME: Borun, Michael F. REGISTRATION NUMBER: 25
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TYPE: amino acid
                               APPLICATION NUMBER: 08,
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
            PRIOR APPLICATION DATA:
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Matches 487; Conservative
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US-09-782-642-2
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                                                                                                               Length 487;
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                           Indels
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COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-Feb-2001
CLASSIFICATION: <university control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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                                                                                                               DB 9;
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                                                                                                          100.0%; Score 2507; DB 9;
100.0%; Pred. No. 1.7e-209;
tive 0; Mismatches 0;
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-728-938-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09782642 Patent No. US20020103118A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                               Query Match
Best Local Similarity 100.
Marches 487; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GADVVYK 487
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GADVVYK 487
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US-09-782-642-2
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100.0%; Pred. No. 1.7e-209;
iive 0; Mismatches 0;
                                                                                                       #1.25
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,245
                                                                                                                                                                                                                   TELLING CASTIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RIL-Lauree, Li-Haien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/33565
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-648
TELEPHONE: 312/474-648
INPORMATION FOR SEQ ID NO: 2:
ENGTH: 487 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/742,985
FILING DATE:
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Best Local Similarity 100.
Matches 487; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                             METHODS OF TREATING CONDITIONS ASSOCIATED WITH CORNEAL INJURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2507; DB 9;
100.0%; Pred. No. 1.7e-209;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
PRIOR APPLICATION: 27-Aug-2001
CLASSIFFCATION: AUKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET UNBER: 27129/33006
TELECOMMUICATION INFORMATION:
TELEPRONE: 312/474-6300
TELEFRAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/557,289
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
Sequence 2, Application US/09941198A Patent No. US20020128191A1 GENERAL INFORMATION:
APPLICANT: Scannon, Patrick J. TITLE OF INVENTION: METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 487 amino acids
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                               Borun
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                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                              APPLICANT: Scott, Randal W
APPLICANT: Marra, Marian N
TILE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS
FILE REFERENCE: 1103/113070361
CURRENT APPLICATION NUMBER: US/09/861,400
CURRENT PILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 08/431,517
PRIOR FILING DATE: 1995-05-01
SOFTWARE: PATENTIN NUMBER: 08/21,517
SOFTWARE: PATENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: human BPI amino acid (Figure 5)
                                                                                              ; Sequence 15, Application US/09861400
; Patent No. US20020146761A1
; GENERAL INFORMATION:
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; LOCATION: (1)..(31)
; NAME/KEY: CHAIN
; LOCATION: (32)..(487)
US-09-861-400-15
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GADVVYK 487
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ORGANISM: human
                                                                                  US-09-861-400-15
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Sequence 2, Application US/09866514;
Patent No. US20020137050A1
GENERAL INFORMATION:
APPLICANT: Elsbach and Weiss
TITLE OF INVENTION: THERAPEUTIC USES OF BACTERICIDAL/PERWEABILITY-INCREASING
TITLE OF INVENTION: PROTEIN FRAGMENTS
FILE REFERENCE: 28297/32248B
CURRENT FILING DATE: 1999-05-10
PRIOR APPLICATION NUMBER: US/9866,514
CURRENT FILING DATE: 1999-05-10
PRIOR APPLICATION NUMBER: 09/309,217
PRIOR APPLICATION NUMBER: 09/309,217
SEQ. ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO. 2
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Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-514-2
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US-09-866-514-2
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STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver.
SEQ ID NO 3
LENGTH: 487
                                                               TYPE: PRT
ORGANISM: Homo sapiens
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US-09-416-828-2
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                                                            APPLICATE: Little, II, Roger G.

TITLE OF INVENTION: IDENTIFICATION OF NOVEL ANTIMICROBIAL AGENTS USING TITLE OF INVENTION: IDENTIFICATION OF NOVEL ANTIMICROBIAL AGENTS USING TITLE OF INVENTION: METABOLIC OXIDATION-REDUCTION INDICATOR DYES CURRENT APPLICATION NUMBER: US/09/746,311

CURRENT FILING DATE: 2001-09-10

PRIOR FAPLICATION NUMBER: 60/143,290

PRIOR FILING DATE: 1999-07-12

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN Ver. 2.1
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100.0%; Pred. No. 1.7e-209;
tive 0; Mismatches 0;
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Publication No. US20030166528A1
GENERAL INFORMATION:
APPLICANT: Lin, Jong Jye
ITLE OF INVENTION: Antifungal Compound
FILE REFERENCE: 27129/37753
CURRENT APPLICATION NUMBER: US/09/975,638B
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-11
                US/09746311
             Sequence 2, Application US/0974 Publication No. US20030017143A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 487; Conservative
                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-311-2
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US-09-975-638B-3
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Publication No. US20030171265A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method of Treating Conditions Associated with
TITLE OF INVENTION: Intestinal Ischemia/Reperfusion
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: G300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
                                                                 ;
0
Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,828
FILING DATE:
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HSNIGPPVELLODIMNYIVPILVLPRVNEKLOKGFPLPTPARVQLYNVVLQPHQNFLLF 480
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                                                       STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE:
COMPUTER: DEACH IN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,234
FILLING DATE: 10-0an-2000
CLASSIFCATION: 514
PRIOR APPLICATION DATA:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 2507; DB 10; Best Local Similarity 100.0%; Pred. No. 1.7e-209; Matches 487; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/34309
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/962,217
FILING DATE: «Uhknown»
APPLICATION NUMBER: 08/742,986
FILING DATE: 1-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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LENGTH: 487 amino acids
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INFORMATION FOR SEQ ID NO: 2:
                      STREET: 6300 S
CITY: Chicago
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Publication No. US20030194377A1
GENERAL INFORMATION:
APPLICANT: Carroll, Stephen F.
Scannon, Patrick J.
Gavit, Partick J.
Gavit, Pertick J.
TITLE OF INVENTION: IMPROVED THERAPEUTIC USES OF BPI PROTEIN
TITLE OF INVENTION: INPROVED THERAPEUTIC SATIENTS
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                                                                                                                                                    27129/32043
                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/756,16.
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Osffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 2712;
TELECHONE: 312/474-6300
TELECHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                   : 487 amino acids
amino acid
                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 487; Conservative
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                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-09-416-828-2
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GADVVYK 487
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Best Local Similarity
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US-09-480-234-2
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Search completed: October 21, 2005, 11:37:01 Job time: 174.285 secs

From:

Chan, Christina

Sent: To: Thursday, October 20, 2005 5:15 PM Mitra, Rita; STIC-Biotech/ChemLib

Subject:

RE: SEQ search request 10/629516

## Please rush. Thanks Chris

## Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

OCT 21 2005
LECH/CHEN. DIVIL
(STIC)

-----Original Message-----

From:

Mitra, Rita

Sent:

Thursday, October 20, 2005 4:16 PM

To:

Chan, Christina

Subject:

SEQ search request 10/629516

I need your approval for this search request.

I would like to request an expedited sequence search for this case because it is due this bi-week. Please search commercial and published patent databases.

10/629516

SEQ ID NO: 2,

SEQ ID NO: 2, amino acids 10-193

Please print out the result.

Thanks. Rita

Rita Mitra, Ph.D.
Patent Examiner, Art Unit 1653
U.S. Patent and Trademark Office
Remsen Bldg, Rm 3B65
Alexandria, VA 22313
3070
(571)272-0954

E-mail: rita.mitra@uspto.gov

*******
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

Type of Search				
NA#	AA#:			
	Oligomer:			
Encode/Tra	nsl:			
Structure #	:Text:			
Inventor:	Litigation:			

*******

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Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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